GenCore version 5.1.6

protein - protein search, using sw model

n on: October 27, 2004, 16:51:34 ; Search time 23.1174 Seconds
(without alignments)
665.548 Million cell updates/sec

tle: US-10-000-439-3
rfect score: 1260
quence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNHYQQRSLSLSPGK 232

oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 478139 seqs, 66318000 residues

tal number of hits satisfying chosen parameters: 478139

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

tabase : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	1225	97.2	232	2	US-08-595-043A-50	Sequence 50, Appl
2	1225	97.2	232	4	US-09-968-362A-26	Sequence 26, Appl
3	1225	97.2	331	3	US-09-178-869-2	Sequence 2, Appli
4	1225	97.2	331	4	US-09-761-413-2	Sequence 2, Appli
5	1225	97.2	360	3	US-09-180-100-11	Sequence 11, Appl
6	1225	97.2	371	1	US-08-236-311-7	Sequence 7, Appli
7	1225	97.2	371	3	US-08-457-918-7	Sequence 7, Appli
8	1225	97.2	371	4	US-10-157-408-7	Sequence 7, Appli
9	1225	97.2	376	3	US-09-180-100-22	Sequence 22, Appl
10	1225	97.2	396	2	US-08-784-512-3	Sequence 3, Appli
11	1225	97.2	396	3	US-09-176-228-3	Sequence 3, Appli
12	1225	97.2	424	5	PCT-US95-03866-12	Sequence 12, Appl
13	1225	97.2	424	5	PCT-US95-03866-14	Sequence 14, Appl
14	1225	97.2	437	5	PCT-US96-10043-11	Sequence 11, Appl
15	1225	97.2	442	4	US-08-472-888A-7	Sequence 7, Appli
16	1225	97.2	442	5	PCT-US96-10043-9	Sequence 9, Appli
17	1225	97.2	446	3	US-08-397-411-7	Sequence 7, Appli
18	1225	97.2	449	1	US-08-458-516-13	Sequence 13, Appl
19	1225	97.2	459	1	US-08-157-101A-7	Sequence 7, Appli
20	1225	97.2	467	4	US-08-030-175-41	Sequence 41, Appl
21	1225	97.2	467	4	US-08-030-175-42	Sequence 42, Appl
22	1225	97.2	475	4	US-09-740-002-27	Sequence 27, Appl
23	1225	97.2	476	2	US-08-378-939-10	Sequence 10, Appl
24	1225	97.2	476	3	US-08-487-550-4	Sequence 4, Appli
25	1225	97.2	476	3	US-08-487-550-12	Sequence 12, Appl
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27	1225	97.2	476	4	US-09-526-098-12	Sequence 12, Appl
28	1225	97.2	476	4	US-09-383-916-4	Sequence 4, Appli
29	1225	97.2	476	4	US-09-383-916-12	Sequence 12, Appl
30	1225	97.2	478	3	US-08-487-550-8	Sequence 8, Appli
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33	1225	97.2	497	4	US-09-499-846-6	Sequence 6, Appli
34	1225	97.2	525	4	US-09-499-846-4	Sequence 4, Appli
35	1225	97.2	547	4	US-09-746-359A-54	Sequence 54, Appl
36	1225	97.2	567	4	US-09-825-561A-16	Sequence 16, Appl
37	1225	97.2	571	4	US-09-746-359A-53	Sequence 53, Appl
38	1225	97.2	592	4	US-09-313-942-8	Sequence 8, Appli
39	1225	97.2	622	4	US-09-499-846-2	Sequence 2, Appli
40	1225	97.2	859	4	US-09-313-942-7	Sequence 7, Appli
41	1225	97.2	951	4	US-09-313-942-9	Sequence 9, Appli
42	1224	97.1	475	4	US-09-740-002-25	Sequence 25, Appl
43	1221	96.9	462	4	US-09-289-942A-7	Sequence 7, Appli
44	1220	96.8	254	2	US-08-284-391B-33	Sequence 33, Appl
45	1220	96.8	254	3	US-09-218-950-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SGARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-043A-50

Query Match 97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 3.4e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232


RESULT 2
US-09-968-362A-26
; Sequence 26, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
;  APPLICANT: Sun, Lee-Hwei K
;  APPLICANT:  Sun, Bill
;  APPLICANT:  Sun, Cecily R
;  TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor
;  TITLE OF INVENTION:  increased biological activities
;  FILE REFERENCE: 03SUN2001
;  CURRENT APPLICATION NUMBER: US/09/968,362A
;  CURRENT FILING DATE:  2001-10-01
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 232
;   TYPE: PRT
;   ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-968-362A-26

  Query Match             97.2%;  Score 1225;  DB 4;  Length 232;
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  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

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Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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RESULT 3
US-09-178-869-2
; Sequence 2, Application US/09178869B
; Patent No. 6197294
; GENERAL INFORMATION:
;  APPLICANT: Tao, Weng
;  APPLICANT: Wong, Shou
;  APPLICANT: Hickey, William F
;  APPLICANT: Hammang, Joseph P.
;  APPLICANT: Baetge, E. Edward
;  TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
;  FILE REFERENCE: 17810-043
;  CURRENT APPLICATION NUMBER: US/09/178,869B
;  CURRENT FILING DATE: 1998-10-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 331
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-178-869-2

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  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

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RESULT 4
US-09-761-413-2
; Sequence 2, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
;  APPLICANT: Tao, Weng
;  APPLICANT:  Wong, Shou
;  APPLICANT:  Hickey, William F
;  APPLICANT:  Hammang, Joseph P.
;  APPLICANT:  Baetge, E. Edward
;  TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
;  FILE REFERENCE: 17810-043
;  CURRENT APPLICATION NUMBER: US/09/761,413
;  CURRENT FILING DATE:  2001-01-16
;  PRIOR APPLICATION NUMBER: US/09/178,869
;  PRIOR FILING DATE: 1998-10-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 331
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-761-413-2

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  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

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RESULT 5
US-09-180-100-11
; Sequence 11, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA, No. 6306395io
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APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
-09-180-100-11

Query Match 97.2%; Score 1225; DB 3; Length 360;
Best Local Similarity 97.0%; Pred. No. 6.3e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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SULT 6
-08-236-311-7
Sequence 7, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987

; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-236-311-7

Query Match 97.2%; Score 1225; DB 1; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
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Db        260 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 319

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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RESULT 7
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988

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;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/104329
;       FILING DATE:  02-OCT-1987
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kubinec, Jeffrey S.
;       REGISTRATION NUMBER:  36,575
;       REFERENCE/DOCKET NUMBER:  P0444P1C3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-8228
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  371 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-457-918-7

  Query Match             97.2%;  Score 1225;  DB 3;  Length 371;
  Best Local Similarity   97.0%;  Pred. No. 6.6e-116;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

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Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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Db        200 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 319

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        320 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371


RESULT 8
US-10-157-408-7
; Sequence 7, Application US/10157408
; Patent No. 6710169
;   GENERAL INFORMATION:
;       APPLICANT: Capon, Daniel J.
;                  Gregory, Timothy J.
;       TITLE OF INVENTION: Adheson Variants
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 460 Point San Bruno Blvd
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: patin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/157,408
;            FILING DATE: 28-May-2002
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/457,918
;            FILING DATE: 1-JUN-1995
;            APPLICATION NUMBER: 08/236311
;            FILING DATE: 02-MAY-1994
;            APPLICATION NUMBER: 07/936190
;            FILING DATE: 26-AUG-1992
;            APPLICATION NUMBER: 07/842777
;            FILING DATE: 18-FEB-1992
;            APPLICATION NUMBER: 07/250785
;            FILING DATE: 28-SEP-1988
;            APPLICATION NUMBER: 07/104329
;            FILING DATE: 02-OCT-1987
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kubinec, Jeffrey S.
;            REGISTRATION NUMBER: 36,575
;            REFERENCE/DOCKET NUMBER: P0444P1C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415/225-8228
;            TELEFAX: 415/952-9881
;            TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 371 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-157-408-7

  Query Match             97.2%;  Score 1225;  DB 4;  Length 371;
  Best Local Similarity   97.0%;  Pred. No. 6.6e-116;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||||:|:|||||||||||||||||||||||
Db        200 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 319

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        320 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371


RESULT 9
US-09-180-100-22
; Sequence 22, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA, No. 6306395io
;  APPLICANT: NAGATA, Shigekazu
;  TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
;  FILE REFERENCE: 1110-207P
;  CURRENT APPLICATION NUMBER: US/09/180,100
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: PCT/JP97/01502
;  EARLIER FILING DATE: 1997-05-01
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 376
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-180-100-22

  Query Match             97.2%;  Score 1225;  DB 3;  Length 376;
  Best Local Similarity   97.0%;  Pred. No. 6.8e-116;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 204

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||||:|:|||||||||||||||||||||||
Db        205 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 264
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       121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       265 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 324

       181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
           ||||| |||||||||||||||||||||||||||||||| |:||||||||
       325 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 376


SULT 10
-08-784-512-3
Sequence 3, Application US/08784512
Patent No. 5872209
 GENERAL INFORMATION:
   APPLICANT:  BARTNIK, Eckart
   APPLICANT:  EIDENMUELLER, Bernd
   APPLICANT:  BUETTNER, Frank
   APPLICANT:  CATERSON, Bruce
   APPLICANT:  HUGHES, Clare
   TITLE OF INVENTION:  An artificial recombinant substrate (rAGG 1)
   TITLE OF INVENTION:  and native aggrecan to study the proteolytic activity of
   TITLE OF INVENTION:  "Aggrecanase" in cell culture systems
   NUMBER OF SEQUENCES:  4
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Foley & Lardner
     STREET:  Suite 500, 3000 K Street, N.W.
     CITY:  Washington, D.C.
     COUNTRY:  USA
     ZIP:  20007-5109
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.25
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  US/08/784,512
     FILING DATE:  17-JAN-1997
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  EP 96100682.2
     FILING DATE:  18-JAN-1996
   ATTORNEY/AGENT INFORMATION:
     NAME:  GRANADOS, Patricia D.
     REGISTRATION NUMBER:  33,683
     REFERENCE/DOCKET NUMBER:  18748/311
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (202)672-5300
     TELEFAX:  (202)672-5399
     TELEX:  904136
  INFORMATION FOR SEQ ID NO:  3:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  396 amino acids
      TYPE:  amino acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
    MOLECULE TYPE:  protein
    FEATURE:
      NAME/KEY:  Protein
      LOCATION:  1..396
3-08-784-512-3

 Query Match             97.2%;  Score 1225;  DB 2;  Length 396;
 Best Local Similarity   97.0%;  Pred. No. 7.3e-116;
 Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

y          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        165 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 224

y         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
             |||||||||| |||||||||||||||||||||:|:||||||||||||||||||||||||
b        225 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 284
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Qy       121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       285 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 344

Qy       181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
             ||||| |||||||||||||||||||||||||||||||| |:||||||||
Db       345 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 396


RESULT 11
US-09-176-228-3
; Sequence 3, Application US/09176228
; Patent No. 6180334
;  GENERAL INFORMATION:
;    APPLICANT:  BARTNIK, Eckart
;    APPLICANT:  EIDENMUELLER, Bernd
;    APPLICANT:  BUETTNER, Frank
;    APPLICANT:  CATERSON, Bruce
;    APPLICANT:  HUGHES, Clare
;    TITLE OF INVENTION:  An artificial recombinant substrate (rAGG 1)
;    TITLE OF INVENTION:  and native aggrecan to study the proteolytic activity of
;    TITLE OF INVENTION:  "Aggrecanase" in cell culture systems
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  Suite 500, 3000 K Street, N.W.
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/176,228
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/784,512
;      FILING DATE:  17-JAN-1997
;      APPLICATION NUMBER:  EP 96100682.2
;      FILING DATE:  18-JAN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GRANADOS, Patricia D.
;      REGISTRATION NUMBER:  33,683
;      REFERENCE/DOCKET NUMBER:  18748/311
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  396 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..396
US-09-176-228-3

  Query Match             97.2%;  Score 1225;  DB 3;  Length 396;
  Best Local Similarity   97.0%;  Pred. No. 7.3e-116;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       165 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 224

Qy        61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
             |||||||||| |||||||||||||||||||||:|:||||||||||||||||||||||||
Db       225 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 284
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Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 344

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        345 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 396


RESULT 12
PCT-US95-03866-12
; Sequence 12, Application PC/TUS9503866
;  GENERAL INFORMATION:
;    APPLICANT:  CytoMed, Inc. (all states except US)
;    APPLICANT:  Nocka, Karl (US only)
;    APPLICANT:  Lobell, Robert B (US only)
;    TITLE OF INVENTION:  STABILIZED DIMER OF KIT LIGAND AND
;    TITLE OF INVENTION:  FLT-3/FLK-2 LIGAND
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/03866
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/220,379
;      FILING DATE:  28-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr, James F
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  CytoMed/2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-596-9000
;      TELEFAX:  212-596-9090
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  424 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-03866-12

  Query Match             97.2%;  Score 1225;  DB 5;  Length 424;
  Best Local Similarity   97.0%;  Pred. No. 8e-116;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 252

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||:|:||||||||||||||||||||||||||
Db        253 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 312

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 372

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        373 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 424


RESULT 13
PCT-US95-03866-14
; Sequence 14, Application PC/TUS9503866
;  GENERAL INFORMATION:
;    APPLICANT:  CytoMed, Inc. (all states except US)
;    APPLICANT:  Nocka, Karl (US only)
;    APPLICANT:  Lobell, Robert B (US only)
;    TITLE OF INVENTION:  STABILIZED DIMER OF KIT LIGAND AND
;    TITLE OF INVENTION:  FLT-3/FLK-2 LIGAND
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/03866
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/220,379
;      FILING DATE:  28-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr, James F
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  CytoMed/2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-596-9000
;      TELEFAX:  212-596-9090
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  424 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-03866-14

  Query Match             97.2%;  Score 1225;  DB 5;  Length 424;
  Best Local Similarity   97.0%;  Pred. No. 8e-116;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 252

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||||||:|:||||||||||||||||||||||
Db        253 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 312

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 372

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        373 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 424


RESULT 14
PCT-US96-10043-11
; Sequence 11, Application PC/TUS9610043
;  GENERAL INFORMATION:
;    APPLICANT:  The General Hospital Corporation
;    TITLE OF INVENTION:  P-SELECTIN LIGANDS AND RELATED MOLECULES
```

```
   TITLE OF INVENTION:  AND METHODS
   NUMBER OF SEQUENCES:  14
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  Fish & Richardson P.C.
     STREET:  225 Franklin Street
     CITY:  Boston
     STATE:  MA
     COUNTRY:  USA
     ZIP:  02210-2804
   COMPUTER READABLE FORM:
     MEDIUM TYPE:  Floppy disk
     COMPUTER:  IBM PC compatible
     OPERATING SYSTEM:  PC-DOS/MS-DOS
     SOFTWARE:  PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER:  PCT/US96/10043
     FILING DATE:
     CLASSIFICATION:
   PRIOR APPLICATION DATA:
     APPLICATION NUMBER:  US 60/000,213
     FILING DATE:  14-JUN-1995
     CLASSIFICATION:
   ATTORNEY/AGENT INFORMATION:
     NAME:  Lech, Karen F.
     REGISTRATION NUMBER:
     REFERENCE/DOCKET NUMBER:  00786/284001
   TELECOMMUNICATION INFORMATION:
     TELEPHONE:  617/542-5070
     TELEFAX:  617/542-8906
     TELEX:  200154
 INFORMATION FOR SEQ ID NO:  11:
   SEQUENCE CHARACTERISTICS:
     LENGTH:  437 amino acids
     TYPE:  amino acid
     STRANDEDNESS:  not relevant
     TOPOLOGY:  linear
   MOLECULE TYPE:  protein
'T-US96-10043-11

Query Match             97.2%;  Score 1225;  DB 5;  Length 437;
Best Local Similarity   97.0%;  Pred. No. 8.4e-116;
Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        206 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 265

         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
            |||||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||
        266 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 325

        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
        326 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 385

        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
            ||||| |||||||||||||||||||||||||||||||| |:||||||||
        386 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 437


ESULT 15
3-08-472-888A-7
 Sequence 7, Application US/08472888A
 Patent No. 6613746
  GENERAL INFORMATION:
    APPLICANT:  Seed, Brian
    APPLICANT:  Walz, Gerd
    TITLE OF INVENTION:  AGP-ANTIBODY FUSION PROTEINS
    TITLE OF INVENTION:  AND RELATED MOLECULES AND METHODS
    NUMBER OF SEQUENCES:  9
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Clark & Elbing LLP
      STREET:  176 Federal Street
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02110
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/472,888A
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/618,314
;       FILING DATE:  23-NOV-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Elbing, Karen L
;       REGISTRATION NUMBER:  35,238
;       REFERENCE/DOCKET NUMBER:  00786/258001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-428-0200
;       TELEFAX:  617-428-7045
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  442 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-472-888A-7

  Query Match             97.2%;  Score 1225;  DB 4;  Length 442;
  Best Local Similarity   97.0%;  Pred. No. 8.5e-116;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 270

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||
Db        271 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 330

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 390

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||| |:||||||||
Db        391 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 442


Search completed:  October 27, 2004, 17:05:53
Job time :  24.1174 secs
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GenCore version 5.1.6

d protein - protein search, using sw model

un on: October 27, 2004, 16:51:09 ; Search time 28.7722 Seconds
(without alignments)
1103.547 Million cell updates/sec

itle: US-10-000-439-2
erfect score: 1764
equence: 1 ASTKGPSVFPLAPSSKSTSG.....MHEALHNHYQQRSLSLSPGK 330

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

earched: 283416 seqs, 96216763 residues

otal number of hits satisfying chosen parameters: 283416

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description
1	1729	98.0	330	1	GHHU	Ig gamma-1 chain C
2	1592.5	90.3	377	2	A23511	Ig gamma-3 chain C
3	1590.5	90.2	377	2	A60764	Ig gamma-3 chain C
4	1566	88.8	326	1	G2HU	Ig gamma-2 chain C
5	1552.5	88.0	327	1	G4HU	Ig gamma-4 chain C
6	1225.5	69.5	374	2	S69339	Ig heavy chain V r
7	1225	69.4	328	2	I47159	Ig gamma 2a chain
8	1222	69.3	255	4	S31866	Ig gamma-1 chain C
9	1219	69.1	328	2	I47160	Ig gamma 2b chain
10	1216	68.9	234	2	PT0207	Ig gamma chain C r
11	1193	67.6	328	2	I47158	Ig gamma 1 chain c
12	1192.5	67.6	323	1	GHRB	Ig gamma chain C r
13	1189	67.4	328	2	I47161	Ig gamma 3 chain c
14	1174.5	66.6	329	1	G2GP	Ig gamma-2 chain C
15	1163.5	66.0	472	2	S31459	Ig gamma-1 chain -
16	1144.5	64.9	470	2	S22080	Ig heavy chain pre
17	1125.5	63.8	308	2	C30554	Ig heavy chain C r
18	1123	63.7	289	1	G3HUWI	Ig gamma-3 heavy c
19	1117.5	63.4	333	2	PS0018	Ig gamma-2b chain
20	1116	63.3	444	2	PC4436	monoclonal antibod
21	1114	63.2	326	2	PS0017	Ig gamma-1 chain C
22	1109	62.9	324	1	G1MS	Ig gamma-1 chain C
23	1108	62.8	329	1	G3MSC	Ig gamma-3 chain C
24	1104	62.6	393	1	G1MSM	Ig gamma-1 chain C
25	1097	62.2	398	1	G3MSM	Ig gamma-3 chain C
26	1093	62.0	330	1	G2MSA	Ig gamma-2a chain
27	1093	62.0	469	2	S37483	Ig gamma-2a chain
28	1090.5	61.8	335	1	G2MSAB	Ig gamma-2a chain
29	1088	61.7	399	1	G2MSAM	Ig gamma-2a chain
30	1085.5	61.5	329	2	S00847	Ig gamma-2c chain
31	1078	61.1	446	2	S40295	Ig gamma-2a chain
32	1074	60.9	322	2	PS0019	Ig gamma-2a chain
33	1063.5	60.3	327	2	S06611	Ig gamma-2 chain C
34	1054	59.8	405	1	G2MSBM	Ig gamma-2b chain
35	1039	58.9	475	2	S01321	Ig gamma-2b chain
36	1036.5	58.8	474	1	G2MS11	Ig gamma-2b chain
37	1028	58.3	277	2	I47162	Ig gamma 4 chain c
38	669	37.9	180	2	I46732	Ig gamma heavy cha
39	648.5	36.8	548	2	S38864	Ig epsilon chain C
40	549	31.1	249	2	S69340	Ig heavy chain VHI
41	547	31.0	218	2	A36040	Ig heavy chain V-I
42	547	31.0	549	2	S04845	Ig heavy chain pre
43	542	30.7	152	2	S14236	Ig gamma-1 chain C
44	534	30.3	220	2	A49444	Ig gamma-1 heavy c
45	532	30.2	241	2	S69131	Ig heavy chain (DO

ALIGNMENTS

RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, 2
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a s
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequenc
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,'
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 98.0%; Score 1729; DB 1; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.4e-112;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:||||||||||||||||||||||||||| ||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 1592.5; DB 2; Length 377;
Best Local Similarity 80.1%; Pred. No. 7.7e-103;
Matches 302; Conservative 13; Mismatches 15; Indels 47; Gaps 1;

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Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              |||||||||||||| |:|||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV---------------------- 98
              |||||||||||||||||||| |||||||||||||||:|
Db         61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

Qy         99 -------------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 133
                                       ||||||    || ||||||||||||||||||||||
Db        121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy        134 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLH 193
              |||||||||||||||||||||:| |||||||||| ||||||||||:||||||||||
Db        181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy        194 QNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVK 253
              |:|:|||||||||||||||||||| | ||||||||||||:|:||||||||||
Db        241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

Qy        254 GFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 313
              |||||||||||||:|||||| ||||:||| ||||||||||||||||||:||||||||
Db        301 GFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE 360

Qy        314 ALHNHYQQRSLSLSPGK 330
              |||| : |:||||||||
Db        361 ALHNRFTQKSLSLSPGK 377
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RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conver
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin

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:20-85/Domain: immunoglobulin homology <IMM>

 Query Match             90.2%;  Score 1590.5;  DB 2;  Length 377;
 Best Local Similarity   80.1%;  Pred. No. 1.1e-102;
 Matches  302;  Conservative   13;  Mismatches   15;  Indels   47;  Gaps    1;

/          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||| |:|||||||||||||||||||||||||||||||||||||||||||
)          1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

/         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV---------------------- 98
              ||||||||||||||||||| |||||||||||||:|
)         61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

/         99 -------------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 133
                                       ||||||    || ||||||||||||||||||||||
)        121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

/        134 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLH 193
              |||||||||||||||||||||:| |||||||||| ||||||||||:||||||||||
)        181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

/        194 QNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVK 253
              |:|:|||||||||||||||||||| | ||||||||||||:|:||||||||||||
)        241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

/        254 GFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 313
              ||||||||||||:|||||||| |||||||| |||||||:|||||||||:||||||||||
)        301 GFYPSDIAVEWESSGQPENNYNTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE 360

/        314 ALHNHYQQRSLSLSPGK 330
              |||| : |:||||||||
)        361 ALHNRFTQKSLSLSPGK 377


ESULT 4
2HU
g gamma-2 chain C region - human
;Species: Homo sapiens (man)
;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
;Accession: A93906; A92809; A90752; A93132; A02148
;Ellison, J.; Hood, L.
roc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
;Reference number: A93906; MUID:82197621; PMID:6804948
;Accession: A93906
;Molecule type: DNA
;Residues: 1-326 <ELL>
;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; P
;Note: Lys-326 is probably removed posttranslationally
;Wang, A.C.; Tung, E.; Fudenberg, H.H.
. Immunol. 125, 1048-1054, 1980
;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
;Reference number: A92809; MUID:81007873; PMID:6774012
;Contents: myeloma protein Til
;Accession: A92809
;Molecule type: protein
;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
;Note: Trp-156 is at or near the complement-binding site
;Connell, G.E.; Parr, D.M.; Hofmann, T.
an. J. Biochem. 57, 758-767, 1979
;Title: The amino acid sequences of the three heavy chain constant region domains of a
;Reference number: A90752; MUID:80001357; PMID:113060
;Contents: myeloma protein Zie
;Accession: A90752
;Molecule type: protein
;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
;Note: this sequence has since been revised
;Hofmann, T.; Parr, D.M.
ol. Immunol. 16, 923-925, 1979
;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
;Reference number: A93132; MUID:80114419; PMID:118920
;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             88.8%;  Score 1566;  DB 1;  Length 326;
  Best Local Similarity   89.1%;  Pred. No. 4.4e-101;
  Matches  294;  Conservative   15;  Mismatches   17;  Indels    4;  Gaps    2;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||| |:||| ||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              |||||||||||||: ||||| |||:|||||||||| || | | :  ||||||| : |
Db         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVE---CPPCPAPP-VAG 116

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||:|||||||||||| ||||||||:|
Db        117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||:|||||||:||:|:|||||||||||| |||||||||| | ||||||||||||:|
Db        177 STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE 236

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              :||||||||||||||||||||||||||||||||||||:||| ||||||||||||||||
Db        237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW 296

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        297 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326


RESULT 5
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
```

```
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             88.0%;  Score 1552.5;  DB 1;  Length 327;
  Best Local Similarity   88.8%;  Pred. No. 3.8e-100;
  Matches  293;  Conservative   15;  Mismatches   19;  Indels    3;  Gaps    1;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              |||||||||||||  |:|||  ||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||:|| |||:||||||||:|| |      || ||||| |||
Db         61 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG 117

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||| |||||:|||||||||||| ||||||||:|
Db        118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:||||||||||| ||: |||||||| ||||||||||||::|
Db        178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              :|||||||||||||||||||||||||||||||||||||| |||||||:||||||||
Db        238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 297

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |:|||||||||||||||| |:||||| ||
Db        298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327


RESULT 6
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

  Query Match             69.5%;  Score 1225.5;  DB 2;  Length 374;
  Best Local Similarity   87.1%;  Pred. No. 1.8e-77;
  Matches  230;  Conservative    6;  Mismatches   17;  Indels   11;  Gaps    2;

Qy         78 TQTYICNVN----------HK-PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF 126
              | || |  :          |    | |    ||||||||||||||||||||||||||||
Db        111 TATYYCGYSVEGYGQGYRFHSWGQGTLVTVSSEPKSCDKTHTCPPCPAPELLGGPSVFLF 170

Qy        127 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVV 186
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        171 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 230

Qy        187 SVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQV 246
              ||||||||:|:|||||||||||||||||||||||||||| ||||||||||||||:|:|||||
Db        231 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV 290

Qy        247 SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVF 306
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        291 SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF 350

Qy        307 SCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||| |:||||||||
Db        351 SCSVMHEALHNHYTQKSLSLSPGK 374


RESULT 7
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             69.4%;  Score 1225;  DB 2;  Length 328;
  Best Local Similarity   67.5%;  Pred. No. 1.7e-77;
  Matches  224;  Conservative   46;  Mismatches   56;  Indels    6;  Gaps    2;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              |    |||:|||| |: |||   |||||   ||||||||:||||||:|||| |
Db          1 APKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPVTVTWNSGALSSGVHTFPSVLQPS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              |||||||:||||:||| :::| |||||  : |||||:|  |:       || | :|    |
Db         61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----G 116

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||:|||||||||||||:|||||||| |:|||:|:|||||||||  :|:|:|||:|
Db        117 PSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFN 176
```

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        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
            ||||||||| : ||:|:||||:||||:|| ||||| : ||||| | |||||||||| :|
        177 STYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE 236

        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGSFFLYSKLTVDKS 298
            |::::||:|||| |||| || |||: ||| || ||:|||| | |::||||| :|||:
        237 LSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKA 296

        299 RWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
             || | :| |:|||||||||| |:|:| :|||
        297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328


SULT 8
1866
 gamma-1 chain C region - synthetic
Species: synthetic
Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
Accession: S31866
Filpula, D.
bmitted to the EMBL Data Library, February 1993
Description: Screeing method for protein-protein interactions of cloned gene products.
Reference number: S31866
Accession: S31866
Molecule type: mRNA
Residues: 1-255 <FIL>
Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
Keywords: immunoglobulin
1-22/Region: Escherichia coli outer membrane protein A precursor
23-255/Region: human Ig gamma-1 chain C region

Query Match             69.3%;  Score 1222;  DB 4;  Length 255;
Best Local Similarity   94.6%;  Pred. No. 2e-77;
Matches  226;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

         92 TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 151
            |     || ||||||||||||||||||||||||||||||||||||||||||||||||||||
         17 TVAQADVESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 76

        152 EDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKAL 211
            |||||||||||||||| |||||||||||||||||||||||:|:|||||||||||||||
         77 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 136

        212 PAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 271
            |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
        137 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196

        272 NNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
            |||||||||||| |||||||||||||||||||||||||||||||||| |:||||||||
        197 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255


ESULT 9
47160
g gamma 2b chain constant region - pig (fragment)
;Species: Sus scrofa domestica (domestic pig)
;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
;Accession: I47160
;Kacskovics, I.; Sun, J.; Butler, J.E.
. Immunol. 153, 3565-3573, 1994
;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
;Reference number: I47158; MUID:95015845; PMID:7930579
;Accession: I47160
;Status: preliminary; translated from GB/EMBL/DDBJ
;Molecule type: mRNA
;Residues: 1-328 <KAC>
;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
;Genetics:
;Gene: IgG2b
;Superfamily: immunoglobulin C region; immunoglobulin homology
;133-202/Domain: immunoglobulin homology <IMM>

Query Match             69.1%;  Score 1219;  DB 2;  Length 328;
Best Local Similarity   67.2%;  Pred. No. 4.3e-77;
Matches  223;  Conservative   45;  Mismatches   58;  Indels    6;  Gaps    2;

Qy           1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
               |    | |:|||| : |||   |||||  ||||||||:|||||||||||||||:||| |
Db           1 APKTAPLVYPLAPCGRDTSGPNVALGCLASSYFPEPVTVTWNSGALTSGVHTFPSVLQPS 60

Qy          61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
               |||||||:||||:||| :::| |||||  : |||||:|  |:      || | :|    |
Db          61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----G 116

Qy         121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
               ||||:|||||||||||||:||||||||| |:|||:|:|||||||||  :|:|:|||:|
Db         117 PSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFN 176

Qy         181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
               ||||||||| : ||:|:||||:||||:|| ||||| : ||||| | |||||||||| :|
Db         177 STYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE 236

Qy         241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGSFFLYSKLTVDKS 298
               |::::||:|||| |||| || |||: ||| || ||:|||| | |::||||| :|||:
Db         237 LSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKA 296

Qy         299 RWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                || | :| |:|||||||||| |:|:| :|||
Db         297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328


RESULT 10
PT0207
Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 <EHR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match             68.9%;  Score 1216;  DB 2;  Length 234;
Best Local Similarity   95.7%;  Pred. No. 4.6e-77;
Matches  224;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          90 SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 149
               |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||||
Db           1 SNTKVDKKVEPKSCDTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 60

Qy         150 SHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNK 209
               |||||||||||||||||||||||||||||||||||||||||||:|:||||||||||||
Db          61 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 120

Qy         210 ALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 269
               ||||||||||||| ||||||||||||||||||||||||||||||||||||||||:||
Db         121 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESSGQ 180

Qy         270 PENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRS 323
               |||||||||||||| |||||||||||||||||||||||||||||||| |:|
Db         181 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 234


RESULT 11
I47158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
```

R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C;Genetics:
A;Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 67.6%; Score 1193; DB 2; Length 328;
Best Local Similarity 67.2%; Pred. No. 2.7e-75;
Matches 223; Conservative 42; Mismatches 61; Indels 6; Gaps 3;

```
Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              |    |||:||||  :  ||   |||||   ||||||||:|||||||||||||||:||| |
Db          1 APKTAPSVYPLAPCGRDVSGPNVALGCLASSYFPEPVTVTWNSGALTSGVHTFPSVLQPS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              |||||||:||||:||| :::| |||||  : |||||:|       :  ||| ||  | : |
Db         61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRV---GIHQPQTCPICPGCE-VAG 116

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||:||||||||||||:|||||||||||| |  ||:|:|||||||||  :|:|:|||:|
Db        117 PSVFIFPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEVHTAETRPKEEQFN 176

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||  : ||:|: |||:||||:|  ||||| :|||||  | ||||||||||  :|
Db        177 STYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPPAEE 236

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGSFFLYSKLTVDKS 298
              |:::::|:|||||  |||| || |||:|||| |||  |:|||  |  |:|||||| |||:
Db        237 LSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDGTFFLYSKLAVDKA 296

Qy        299 RWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              ||  |: | |:|||||||||| |:|:|  : ||
Db        297 RWDHGDKFECAVMHEALHNHYTQKSISKTQGK 328
```

RESULT 12
GHRB
Ig gamma chain C region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot
A;Reference number: A91749; MUID:84030930; PMID:6313520
A;Accession: A91749
A;Molecule type: mRNA
A;Residues: 1-323 <BER>
A;Cross-references: UNIPROT:P01870
A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R;Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A;Reference number: A90290; MUID:76135469; PMID:1243651
A;Accession: A90290
A;Molecule type: protein
A;Residues: 1-47,'E',49-71,'PV',72-128 <PRA>
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A;Reference number: A93928; MUID:83299917; PMID:6193512
A;Accession: A93928
A;Molecule type: mRNA
A;Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
A;Cross-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112
A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic mark
R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin
A;Reference number: A90245; MUID:70110015; PMID:5461106
A;Accession: A90245
A;Molecule type: protein
A;Residues: 132-143,'E',145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell
A;Reference number: A94416
A;Accession: A94416
A;Molecule type: protein
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q'
A;Note: this has the e15 allotypic marker, 185-Ala
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology <IM1>
F;130-199/Domain: immunoglobulin homology <IM2>
F;236-303/Domain: immunoglobulin homology <IM3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.6%; Score 1192.5; DB 1; Length 323;
Best Local Similarity 67.9%; Pred. No. 2.9e-75;
Matches 222; Conservative 37; Mismatches 61; Indels 7; Gaps 2;

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Qy          4 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 63
              | ||||||||     |   |  |||||| | ||||||:|||| ||:|| |||:| ||||||
Db          4 KAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLY 63

Qy         64 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 123
              ||||||:| |||    |   ||| |  :|||||| | | :| |    | || ||||||||||
Db         64 SLSSVVSVTSSS---QPVTCNVAHPATNTKVDKTVAPSTCSK----PTCPPPELLGGPSV 116

Qy        124 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTY 183
              |:|||||||||||||||||||||||||| :||||:| ||::  :|   :   ||:|:|||
Db        117 FIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTI 176

Qy        184 RVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTK 243
              |||| | : ||:|: |||:|||| |||||||||||||||: || ||:|||: | |:||:
Db        177 RVVSTLPITHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSS 236

Qy        244 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQG 303
              |||||:: |||||||:|||| ||: |:|||||| |||| ||:|||:||:|   | ||:|
Db        237 RSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYNKLSVPTSEWQRG 296

Qy        304 NVFSCSVMHEALHNHYQQRSLSLSPGK 330
              :||:|||||||||||| |:|:| ||||
Db        297 DVFTCSVMHEALHNHYTQKSISRSPGK 323
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RESULT 13
I47161
Ig gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47161
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C;Genetics:
A;Gene: IgG3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

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Query Match             67.4%;  Score 1189;  DB 2;  Length 328;
Best Local Similarity   66.9%;  Pred. No. 5.1e-75;
Matches  222;  Conservative   43;  Mismatches   61;  Indels    6;  Gaps    3;

          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
            |     |||:||||  :  |||   |||||   |||||||::|||||||||||||:||| |
          1 APKTAPSVYPLAPCGRDTSGPNVALGCLASSYFPEPVTMTWNSGALTSGVHTFPSVLQPS 60

         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
            |||||||:||||:|||  :::| |||||   :  |||||:|   |:        || ||  | : |
         61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKT---KPPCPICPGCE-VAG 116

        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
            ||||:|||||||||||:|||||||||||| |   ||:|:|||||||||  :|:|:|||:|
        117 PSVFIFPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEVHTAETRPKEEQFN 176

        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
            |||||||||  :  ||:|:  |||:|||:|  |||||  :|||||   |  ||||||||||  :|
        177 STYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPPAEE 236

        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGSFFLYSKLTVDKS 298
            |:::|::|||| |||| || |||:||||   || ||:||||   |  |:|||||| |||:
        237 LSRSKVTVTCLVIGFYPPDIHVEWKSNGQPEPEGNYRTTPPQQDVDGTFFLYSKLAVDKA 296

        299 RWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
            ||  .|  | |:|||||||||| |:|:| : ||
        297 RWDHGETFECAVMHEALHNHYTQKSISKTQGK 328
```

SULT 14
GP
gamma-2 chain C region - guinea pig
Species: Cavia porcellus (guinea pig)
Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
Accession: A94553; A90352; A90359; A90384; A90385; A02151
Trischmann, T.M.
bmitted to the Atlas, April 1975
Reference number: A94553
Accession: A94553
Molecule type: protein
Residues: 1-3 <TRI>
Cross-references: UNIPROT:P01862
Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
ochemistry 10, 18-25, 1971
Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
Reference number: A90352; MUID:71058471; PMID:5538606
Accession: A90352
Molecule type: protein
Residues: 4-68 <BIR>
Turner, K.J.; Cebra, J.J.
ochemistry 10, 9-17, 1971
Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ami
Reference number: A90359; MUID:71058486; PMID:5538616
Accession: A90359
Molecule type: protein
Residues: 69-133;312-329 <TUR>
Tracey, D.E.; Cebra, J.J.
iochemistry 13, 4796-4803, 1974
Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
Reference number: A90384; MUID:75036072; PMID:4429665
Accession: A90384
Molecule type: protein
Residues: 134-226 <TRA>
Trischmann, T.M.; Cebra, J.J.
iochemistry 13, 4804-4811, 1974
Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
Reference number: A90385; MUID:75036073; PMID:4609467
Accession: A90385
Molecule type: protein
Residues: 227-311 <TR2>
Oliveira, B.; Lamm, M.E.
iochemistry 10, 26-31, 1971
Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.

A;Reference number: A90354; MUID:71058474; PMID:4922544
A;Contents: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;21-81/Domain: immunoglobulin homology <IM1>
F;135-204/Domain: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
F;142-202/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental

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Query Match             66.6%;  Score 1174.5;  DB 1;  Length 329;
Best Local Similarity   68.2%;  Pred. No. 5.2e-74;
Matches  227;  Conservative   31;  Mismatches   66;  Indels    9;  Gaps    4;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              | |  |||||| |   |||    |||||| |||||||| ||||||||||||||||||| |
Db          2 ARTTAPSVFPLAASCVDTSGSMMTLGCLVKGYFPEPVTVKWNSGALTSGVHTFPAVLQ-S 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH--TCPPCPAPELL 118
              |||||:|:|||||   |    ||| |  |:||||| |||    :    ||| || || |
Db         61 GLYSLTSMVTVPSSQKAT----CNVAHPASSTKVDKTVEPIRTPZPBPCTCPKCPPPENL 116

Qy        119 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQ 178
              ||||||:|||||||||||| || ||||||||| ::|||:| |:||   | | :|||| ||
Db        117 GGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKPRVEQ 176

Qy        179 YNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSR 238
              ||:|:|| ||| : ||:|: |||:|||| |||||||||||||| |  || | ||||||||
Db        177 YNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPPSR 236

Qy        239 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSVGSFFLYSKLTVD 296
              |||:|::||:|||:  |:|:|| ||| ||  |  |  || |||: |: ||:|||||||||
Db        237 DELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADGSYFLYSKLTVD 296

Qy        297 KSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPG 329
              || | || |::|||||||||||  |:::| |||
Db        297 KSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
```

RESULT 15
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>

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Query Match             66.0%;  Score 1163.5;  DB 2;  Length 472;
Best Local Similarity   65.7%;  Pred. No. 4.7e-73;
Matches  218;  Conservative   40;  Mismatches   71;  Indels    3;  Gaps    2;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              |||  | |:||      ||     |||||  | ||||||:||||||||||||||:|||| |
Db        142 ASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPVTVTWNSGALTSGVHTFPAILQSS 201

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
```

```
                 ||||||||||||:|: | ||:|||| |  |:|||||:|||   |    |  || ||| ||
Db        202 GLYSLSSVVTVPASTSGAQTFICNVAHPASSTKVDKRVEPGCPDPCKHC-RCPPPELPGG 260

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
                 ||||:|||||||||| || |||||||||||  :||||:|:|:|:|| |||   :|||||||:|
Db        261 PSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEVRTARTKPREEQFN 320

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
                 ||:|||| | : ||:|  |||:|||| |:|||||| :|||: | | |||||| | | ::|
Db        321 STFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAREPQVYVLAPPQEE 380

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSVGSFFLYSKLTVDKS 298
                 |:|: :|:|||| |||| ||||||: |||| |: | ||   ||: ||:||||:| |||:
Db        381 LSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGTTTSQLDADGSYFLYSRLRVDKN 440

Qy        299 RWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                  ||:|: ::| |||||||||| |:|:| |||
Db        441 SWQEGDTYACVVMHEALHNHYTQKSISKPPGK 472
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Search completed: October 27, 2004, 17:04:50
Job time : 30.2722 secs

GenCore version 5.1.6

1 protein - protein search, using sw model

un on: October 27, 2004, 16:32:53 ; Search time 149.733 Seconds
(without alignments)
1268.081 Million cell updates/sec

:tle: US-10-000-439-2
:rfect score: 1764
:quence: 1 ASTKGPSVFPLAPSSKSTSG.....MHEALHNHYQQRSLSLSPGK 330

:oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

:arched: 1825181 seqs, 575374646 residues

:otal number of hits satisfying chosen parameters: 1825181

.nimum DB seq length: 0
:aximum DB seq length: 2000000000

:ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

:tabase : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1729	98.0	330	1	GC1_HUMAN	P01857 homo sapien
2	1729	98.0	407	2	BAC85237	Bac85237 homo sapi
3	1729	98.0	464	2	AAH19337	Aah19337 homo sapi
4	1729	98.0	465	2	Q6GMX6	Q6gmx6 homo sapien
5	1729	98.0	466	2	AAH64496	Aah64496 homo sapi
6	1729	98.0	467	2	BAC85173	Bac85173 homo sapi
7	1729	98.0	468	2	BAC85175	Bac85175 homo sapi
8	1729	98.0	468	2	BAC85444	Bac85444 homo sapi
9	1729	98.0	469	2	Q7Z7P5	Q7z7p5 homo sapien
10	1729	98.0	470	2	Q6PJA4	Q6pja4 homo sapien
11	1729	98.0	470	2	Q7Z5W1	Q7z5w1 homo sapien
12	1729	98.0	470	2	BAC85235	Bac85235 homo sapi
13	1729	98.0	470	2	BAC85387	Bac85387 homo sapi
14	1729	98.0	470	2	AAH62336	Aah62336 homo sapi
15	1729	98.0	470	2	AAH14258	Aah14258 homo sapi
16	1729	98.0	470	2	AAH18747	Aah18747 homo sapi
17	1729	98.0	470	2	AAH25314	Aah25314 homo sapi
18	1729	98.0	471	2	BAC85388	Bac85388 homo sapi
19	1729	98.0	471	2	AAH24289	Aah24289 homo sapi
20	1729	98.0	472	2	BAC85232	Bac85232 homo sapi
21	1729	98.0	472	2	BAC86225	Bac86225 homo sapi
22	1729	98.0	473	2	BAC05013	Bac05013 homo sapi
23	1729	98.0	474	2	BAC85401	Bac85401 homo sapi
24	1729	98.0	474	2	BAC05012	Bac05012 homo sapi
25	1729	98.0	475	2	Q6GMW7	Q6gmw7 homo sapien
26	1729	98.0	475	2	AAH26038	Aah26038 homo sapi
27	1729	98.0	476	2	Q6GMX1	Q6gmx1 homo sapien
28	1729	98.0	476	2	BAC05017	Bac05017 homo sapi
29	1729	98.0	477	2	BAC85394	Bac85394 homo sapi
30	1729	98.0	477	2	BAC85697	Bac85697 homo sapi
31	1729	98.0	477	2	BAC05018	Bac05018 homo sapi
32	1729	98.0	478	2	BAC85174	Bac85174 homo sapi
33	1729	98.0	478	2	BAC85436	Bac85436 homo sapi
34	1729	98.0	478	2	BAC86514	Bac86514 homo sapi
35	1729	98.0	479	2	AAH06402	Aah06402 homo sapi
36	1729	98.0	479	2	AAH14667	Aah14667 homo sapi
37	1728	98.0	474	2	BAC85350	Bac85350 homo sapi
38	1726	97.8	466	2	Q6IN78	Q6in78 homo sapien
39	1726	97.8	472	2	Q6N089	Q6n089 homo sapien
40	1726	97.8	472	2	CAE45781	Cae45781 homo sapi
41	1725	97.8	467	2	AAH37361	Aah37361 homo sapi
42	1725	97.8	470	2	BAC85172	Bac85172 homo sapi
43	1725	97.8	471	2	BAC05014	Bac05014 homo sapi
44	1725	97.8	473	2	Q6P055	Q6p055 homo sapien
45	1725	97.8	473	2	AAH65820	Aah65820 homo sapi

ALIGNMENTS

RESULT 1
GC1_HUMAN
ID GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;

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RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT   characterization of the protein, the L- and H-chains, the cyanogen
RT   bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981).
CC   -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC       G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC       G1M(3) marker and the G1M (non-1) markers.
CC   -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC       116, 198, 269 and 272.
CC   -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC       155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC       268-272.
CC   -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC       residues 198, 267 and 272.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A93433; GHHU.
DR   PDB; 1AJ7; X-ray; H=1-103.
DR   PDB; 1D5B; X-ray; B/H=1-101.
DR   PDB; 1D5I; X-ray; H=1-101.
DR   PDB; 1D6V; X-ray; H=1-101.
DR   PDB; 1DN2; X-ray; A/B=120-326.
DR   PDB; 1E4K; X-ray; A/B=106-329.
DR   PDB; 1FC1; X-ray; A/B=106-329.
DR   PDB; 1FC2; X-ray; D=106-329.
DR   PDB; 1FCC; X-ray; A=121-326.
DR   PDB; 1HZH; X-ray; H/K=1-330.
DR   PDB; 1I7Z; X-ray; B/D=1-103.
DR   PDB; 1IIS; X-ray; A/B=107-330.
DR   PDB; 1IIX; X-ray; A/B=107-330.
DR   PDB; 1L6X; X-ray; A=120-326.
DR   PDB; 1OQX; X-ray; A/B=119-330.
DR   PDB; 2RCS; X-ray; H=1-103.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   3D-structure; Direct protein sequencing; Glycoprotein;
KW   Immunoglobulin C region; Immunoglobulin domain.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       Hinge.
FT   DOMAIN      111    223       CH2.
FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    103       Interchain (with light chain).
FT   DISULFID    109    109       Interchain (with heavy chain).
FT   DISULFID    112    112       Interchain (with heavy chain).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   CARBOHYD    180    180       N-linked (GlcNAc. . .).
FT   VARIANT      97     97       K -> R (in G1M(3) marker).
FT                                /FTId=VAR_003886.
FT   VARIANT     239    239       D -> E (in G1M(non-1) marker).
FT                                /FTId=VAR_003887.
FT   VARIANT     241    241       L -> M (in G1M(non-1) marker).
FT                                /FTId=VAR_003888.
FT   STRAND       23     24
FT   STRAND       26     33
FT   STRAND       38     38
FT   STRAND       41     41
FT   TURN         42     45
FT   TURN         48     49
FT   STRAND       50     52
FT   STRAND       57     58
FT   TURN         59     61
FT   STRAND       62     71
FT   HELIX        73     75
FT   TURN         76     78
FT   STRAND       82     87
FT   TURN         88     91
FT   STRAND       92     97
FT   TURN        102    103
FT   STRAND      122    126
FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    149
FT   STRAND      157    162
FT   TURN        163    164
FT   STRAND      165    167
FT   STRAND      171    172
FT   STRAND      176    177
FT   TURN        179    180
FT   STRAND      183    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    207
FT   TURN        209    210
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    242
FT   STRAND      245    256
FT   STRAND      261    266
FT   TURN        267    268
FT   STRAND      269    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      306    311
FT   TURN        313    314
FT   HELIX       316    318
FT   STRAND      319    324
SQ   SEQUENCE   330 AA;  36106 MW;  3770EE106C2PA33D CRC64;
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Query Match 98.0%; Score 1729; DB 1; Length 330;
Best Local Similarity 97.9%; Pred. No. 1e-117;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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        61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

       121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
       121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

       181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
           ||||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
       181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

       241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
       241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

       301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
           |||||||||||||||||| |:||||||||
       301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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RESULT 2
AC85237
ID   BAC85237    PRELIMINARY;      PRT;   407 AA.
AC   BAC85237;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CDNA FLJ26298 fis, clone DMC07404, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dermoid tumor;
RA   Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA   Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK129809; BAC85237.1; -.
SQ   SEQUENCE   407 AA;  44159 MW;  DB8E4D367B456FCE CRC64;

 Query Match            98.0%;  Score 1729;  DB 2;  Length 407;
 Best Local Similarity  97.9%;  Pred. No. 1.3e-117;
 Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 137

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 197

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        198 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 257

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        258 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 317

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        318 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 377

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        378 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 407
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RESULT 3
AAH19337
ID   AAH19337    PRELIMINARY;      PRT;   464 AA.
AC   AAH19337;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019337; AAH19337.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   464 AA;  50891 MW;  2F80673E74E2A485 CRC64;

  Query Match            98.0%;  Score 1729;  DB 2;  Length 464;
  Best Local Similarity  97.9%;  Pred. No. 1.6e-117;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 194

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 254

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        255 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 314

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        315 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 374

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        375 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 434

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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                   |||||||||||||||||||| |:||||||||
Db        435 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 464


RESULT 4
Q6GMX6
ID   Q6GMX6      PRELIMINARY;      PRT;   465 AA.
AC   Q6GMX6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073766; AAH73766.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51083 MW;  B3A9B7D0FDB1386E CRC64;

  Query Match           98.0%;  Score 1729;  DB 2;  Length 465;
  Best Local Similarity   97.9%;  Pred. No. 1.6e-117;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 195

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 255

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        256 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 315

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||||| ||||||||||||||||||
Db        316 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 375

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        376 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 435

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||||| |:||||||||
Db        436 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 5
AAH64496
ID   AAH64496    PRELIMINARY;      PRT;   466 AA.
AC   AAH64496;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC064496; AAH64496.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   466 AA;  51078 MW;  13F032EDAC9DBC22 CRC64;

  Query Match           98.0%;  Score 1729;  DB 2;  Length 466;
  Best Local Similarity   97.9%;  Pred. No. 1.6e-117;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 196

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 256
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       121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
       257 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 316

       181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
           |||||||||||||:|:|||||||||||||||||||||||||||| ||||||||||||||||
       317 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 376

       241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
       377 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 436

       301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
           |||||||||||||||||| |:||||||||
       437 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466


ESULT 6
AC85173
)  BAC85173    PRELIMINARY;      PRT;   467 AA.
1  BAC85173;
2  02-MAR-2004 (TrEMBLrel. 27, Created)
2  02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
2  02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
3  CDNA FLJ26001 fis, clone DMC07585, highly similar to Ig gamma-1 chain
3  C region.
3  Homo sapiens (Human).
4  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
4  Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
4  NCBI_TaxID=9606;
4  [1]
5  SEQUENCE FROM N.A.
5  TISSUE=Dermoid tumor;
6  Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
6  Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
6  Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
6  Kawakami B., Nagai K., Isogai T., Sugano S.;
7  "NEDO human cDNA sequencing project.";
8  Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
8  EMBL; AK129512; BAC85173.1; -.
9  SEQUENCE   467 AA;  50782 MW;  632AEA2D6CD248F5 CRC64;

 Query Match             98.0%;  Score 1729;  DB 2;  Length 467;
 Best Local Similarity   97.9%;  Pred. No. 1.6e-117;
 Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

         1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

        61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       198 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 257

       121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
       258 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317

       181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
           |||||||||||||:|:|||||||||||||||||||||||||||| ||||||||||||||||
       318 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377

       241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
       378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 437

       301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
           |||||||||||||||||| |:||||||||
       438 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467


ESULT 7
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BAC85175
ID   BAC85175    PRELIMINARY;      PRT;   468 AA.
AC   BAC85175;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CDNA FLJ26006 fis, clone DMC08725, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dermoid tumor;
RA   Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA   Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK129517; BAC85175.1; -.
SQ   SEQUENCE   468 AA;  51266 MW;  11C519D86AE3D44B CRC64;

  Query Match             98.0%;  Score 1729;  DB 2;  Length 468;
  Best Local Similarity   97.9%;  Pred. No. 1.6e-117;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 198

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 258

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        259 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 318

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||||||| ||||||||||||||||
Db        319 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 378

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        379 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 438

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        439 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 468


RESULT 8
BAC85444
ID   BAC85444    PRELIMINARY;      PRT;   468 AA.
AC   BAC85444;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CDNA FLJ27334 fis, clone TMS09201, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymus;
RA   Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
RA   Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA   Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
RA   Sugano S.;
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RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK130844; BAC85444.1; -.
SQ   SEQUENCE   468 AA;  51224 MW;  9280ACAD6817FC20 CRC64;

  Query Match             98.0%;  Score 1729;  DB 2;  Length 468;
  Best Local Similarity   97.9%;  Pred. No. 1.6e-117;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 198

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 258

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        259 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 318

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        319 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 378

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        379 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 438

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        439 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 468


RESULT 9
Q7Z7P5
ID   Q7Z7P5      PRELIMINARY;      PRT;   469 AA.
AC   Q7Z7P5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHG1 protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC051328; AAH51328.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   469 AA;  51395 MW;  C8D5BE12BAAF795C CRC64;

  Query Match             98.0%;  Score 1729;  DB 2;  Length 469;
  Best Local Similarity   97.9%;  Pred. No. 1.6e-117;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 199

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 259

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        260 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 319

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        320 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 379

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        380 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 439

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        440 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 469


RESULT 10
Q6PJA4
ID   Q6PJA4      PRELIMINARY;      PRT;   470 AA.
AC   Q6PJA4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018747; AAH18747.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51715 MW;  7B49556A11FD7D99 CRC64;

Query Match             98.0%;  Score 1729;  DB 2;  Length 470;
Best Local Similarity   97.9%;  Pred. No. 1.6e-117;
Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 260

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||:|:|||||||||||||||||||||||||||| ||||||||||||||
Db        321 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 11
Q7Z5W1
ID   Q7Z5W1      PRELIMINARY;      PRT;   470 AA.
AC   Q7Z5W1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053984; AAH53984.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51204 MW;  778CF34521483E1A CRC64;

  Query Match             98.0%;  Score 1729;  DB 2;  Length 470;
  Best Local Similarity   97.9%;  Pred. No. 1.6e-117;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 260

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||:|:|||||||||||||||||||||||||||| ||||||||||||||
Db        321 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 12
BAC85235
ID   BAC85235    PRELIMINARY;      PRT;   470 AA.
AC   BAC85235;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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DE   CDNA FLJ26276 fis, clone DMC06522, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dermoid tumor;
RA   Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA   Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK129787; BAC85235.1; -.
SQ   SEQUENCE   470 AA;  51090 MW;  460F4717D4528A16 CRC64;

  Query Match             98.0%;  Score 1729;  DB 2;  Length 470;
  Best Local Similarity   97.9%;  Pred. No. 1.6e-117;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 260

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:||||||||||||||||||||||||| ||||||||||||||||
Db        321 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 13
BAC85387
ID   BAC85387    PRELIMINARY;      PRT;   470 AA.
AC   BAC85387;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CDNA FLJ27075 fis, clone SPL02093, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA   Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA   Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK130585; BAC85387.1; -.
SQ   SEQUENCE   470 AA;  51642 MW;  D8C43B61A782293C CRC64;

  Query Match             98.0%;  Score 1729;  DB 2;  Length 470;
  Best Local Similarity   97.9%;  Pred. No. 1.6e-117;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 260

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:||||||||||||||||||||||||| ||||||||||||||||
Db        321 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Db        441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 14
AAH62336
ID   AAH62336    PRELIMINARY;      PRT;   470 AA.
AC   AAH62336;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062336; AAH62336.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51524 MW;  CC861ACD6B7C1CC6 CRC64;
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Query Match           98.0%;  Score 1729;  DB 2;  Length 470;
Best Local Similarity  97.9%;  Pred. No. 1.6e-117;
Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200

         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 260

        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
        261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320

        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
            |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
        321 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380

        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
            |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
        381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440

        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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        441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


ESULT 15
AH14258
ID   AAH14258    PRELIMINARY;      PRT;   470 AA.
AC   AAH14258;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC014258; AAH14258.1; -.
KW   Hypothetical protein.

SQ   SEQUENCE   470 AA;  51514 MW;  BFD56EF8157DBA79 CRC64;

  Query Match           98.0%;  Score 1729;  DB 2;  Length 470;
  Best Local Similarity  97.9%;  Pred. No. 1.6e-117;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 260

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        321 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


Search completed: October 27, 2004, 17:03:55
Job time : 151.733 secs
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GenCore version 5.1.6

l protein - protein search, using sw model

ın on: October 27, 2004, 16:31:18 ; Search time 126.246 Seconds
(without alignments)
937.702 Million cell updates/sec

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:quence: 1 ASTKGPSVFPLAPSSKSTSG.....MHEALHNHYQQRSLSLSPGK 330

:oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

:arched: 2002273 seqs, 358729299 residues

)tal number of hits satisfying chosen parameters: 2002273

.nimum DB seq length: 0
ıximum DB seq length: 2000000000

)st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

ıtabase : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

:sult No.	Score	% Query Match	Length	DB	ID	Description
1	1764	100.0	330	6	AAO19664	Aao19664 Human IgG
2	1729	98.0	330	4	AAB04071	Aab04071 Zcytor 10
3	1729	98.0	330	5	AAM47856	Aam47856 Human Ig-
4	1729	98.0	330	5	AAE21960	Aae21960 Human dea
5	1729	98.0	330	5	ABB81641	Abb81641 Human IgG
6	1729	98.0	330	5	ABB05736	Abb05736 Human imm
7	1729	98.0	330	6	ABP71856	Abp71856 Human IgG
8	1729	98.0	330	6	AAE32915	Aae32915 Human imm
9	1729	98.0	330	6	AAE32627	Aae32627 Human imm
10	1729	98.0	330	6	ABR82103	Abr82103 Human DR6
11	1729	98.0	330	6	AAO31102	Aao31102 Human A2-
12	1729	98.0	330	6	ABR55836	Abr55836 Anti-Ang-
13	1729	98.0	330	6	AAO30893	Aao30893 Human imm
14	1729	98.0	330	7	ADF11389	Adf11389 Anti-OPGL
15	1729	98.0	330	7	ADE97351	Ade97351 Human IgG
16	1729	98.0	330	7	ADF83605	Adf83605 Cytokine
17	1729	98.0	330	7	ADF75001	Adf75001 Human Ig
18	1729	98.0	330	8	ADM41537	Adm41537 Anti-inte
19	1729	98.0	330	8	ADM68911	Adm68911 Human IgG
20	1729	98.0	332	8	ADL35095	Adl35095 Human IgG
21	1729	98.0	333	8	ADJ95912	Adj95912 Human IgG
22	1729	98.0	333	8	ADL22761	Adl22761 Human ant
23	1729	98.0	351	2	AAR43685	Aar43685 Human kap
24	1729	98.0	356	8	ADJ95976	Adj95976 Immunoglo
25	1729	98.0	371	1	AAP91918	Aap91918 Sequence
26	1729	98.0	442	6	ABR39465	Abr39465 Humanised
27	1729	98.0	442	6	ABR39474	Abr39474 Humanised
28	1729	98.0	442	6	ABU08311	Abu08311 Humanised
29	1729	98.0	442	6	ABU08320	Abu08320 Humanised
30	1729	98.0	442	6	ABR39793	Abr39793 Humanised
31	1729	98.0	442	6	ABB80113	Abb80113 Deglycosy
32	1729	98.0	442	6	ABB80109	Abb80109 Heavy cha
33	1729	98.0	442	7	ADE94066	Ade94066 Humanised
34	1729	98.0	442	7	ADE94075	Ade94075 Humanised
35	1729	98.0	442	8	ADN61714	Adn61714 Humanised
36	1729	98.0	444	6	AAE35327	Aae35327 Humanised
37	1729	98.0	444	6	AAE34876	Aae34876 BIWA4/8 a
38	1729	98.0	444	8	ADL15443	Adl15443 Humanised
39	1729	98.0	444	8	ADO00851	Ado00851 Humanised
40	1729	98.0	445	6	AAO31101	Aao31101 Human A2-
41	1729	98.0	445	7	ADF11421	Adf11421 2E11 anti
42	1729	98.0	445	7	ADF11429	Adf11429 18B2 anti
43	1729	98.0	446	7	ADF11425	Adf11425 2D8 anti-
44	1729	98.0	446	7	ADF11437	Adf11437 9H7 anti-
45	1729	98.0	446	7	ADF11433	Adf11433 16E1 anti

ALIGNMENTS

RESULT 1
AAO19664
ID AAO19664 standard; protein; 330 AA.
XX
AC AAO19664;
XX
DT 28-MAR-2003 (first entry)
XX
DE Human IgG1 heavy chain constant region.
XX
KW Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
KW Fcepsilon receptor; autoimmune disease; constant region; heavy chain;
KW antiasthmatic; antiallergic; antiinflammatory; dermatological;
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200288317-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-US013527.
XX
PR 01-MAY-2001; 2001US-00847208.
PR 24-OCT-2001; 2001US-00000439.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Saxon A, Zhang K, Zhu D;
XX
DR WPI; 2003-103456/09.
XX
PT New fusion molecules comprising polypeptide sequences that bind to IgG
PT inhibitory receptor and native IgE receptor, useful for treating IgE-
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
PT autoimmune diseases.
XX
PS Claim 64; Fig 2; 116pp; English.
XX
CC The present invention relates to a fusion molecule comprising a first
CC polypeptide sequence capable of specific binding to a native IgG
CC inhibitory receptor consisting of an immune receptor tyrosine-based
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
CC functionally connected to a second polypeptide sequence capable of
CC specific binding directly or indirectly to a native IgE receptor
CC (FcepsilonR). Also provided are nucleotide sequences encoding such a
CC fusion protein. The fusion molecules and compositions are useful for
CC treating an IgE-mediated biological response, preferably an IgE-mediated

```
CC   hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC   dermatitis, severe food allergies, chronic urticaria, angioedema or
CC   anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC   type-I diabetes mellitus, or multiple sclerosis, and for preventing of,
CC   or symptoms resulting from, a type I hypersensitivity reaction in a
CC   subject receiving immunotherapy. The present sequence is the human IgG1
CC   heavy chain constant region
XX
SQ   Sequence 330 AA;

  Query Match             100.0%;  Score 1764;  DB 6;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-125;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||||||||||||||
Db        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330


RESULT 2
AAB04071
ID   AAB04071 standard; protein; 330 AA.
XX
AC   AAB04071;
XX
DT   11-APR-2001  (first entry)
XX
DE   Zcytor 10::IgG gamma fusion peptide.
XX
KW   zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
KW   binding; detection; modulation; recombinant cell; haematopoietic cell;
KW   lymphoid cell; myeloid cell; lymph; immune system; blood; bone;
KW   inflammatory response; inflammation; spleen; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO200068381-A1.
XX
PD   16-NOV-2000.
XX
PF   11-MAY-2000; 2000WO-US012924.
XX
PR   11-MAY-1999;   99US-00309861.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Foster DC,  Hammond AK,  Lok S;
XX
DR   WPI; 2001-016096/02.
DR   N-PSDB; AAA54473.
XX
PT   New cytokine receptor mouse zcytor 10, useful for detecting ligands that
PT   stimulate proliferation or development of hematopoietic, lymphoid and
PT   myeloid cells.
XX
PS   Example 17; Page 120-121; 134pp; English.
XX
CC   Isolating a nucleotide which encodes the zcytor 10 cytokine receptor
CC   enables the production of recombinant cells expressing the receptor.
CC   Those cells can then be used to detect the presence of a modulator of
CC   zcytor10 protein by culturing the cells in the presence of a test ligand
CC   and comparing levels of activity of mouse zcytor10 in the presence and
CC   absence of the test sample. Similarly, detection of zcytor10 receptor
CC   ligand within a test sample can be achieved. The method comprising
CC   contacting a test sample containing an amino acid sequence from Cys15 or
CC   Gly25 to Pro230 of the zcytor 10 cytokine receptor and detecting the
CC   binding of the polypeptide to a ligand in the sample. Specified peptide
CC   fragments of the zcytor 10 cytokine receptor and the methods described
CC   are used to identify ligands that stimulate the proliferation and/or
CC   development of haematopoietic, lymphoid and myeloid cells. Peptide
CC   fragments of the cytokine receptor are useful for treating lymphoid,
CC   immune, inflammatory, splenic, blood or bone disorders and for generating
CC   antibodies directed against the receptor. A vector expressing a secreted
CC   human zcytor 10 heterodimer is constructed. In this construct the
CC   extracellular cytokine binding domain of zcytor 10 is fused to the heavy
CC   chain of IgG gamma and the extracellular portion of the the heteromeric
CC   cytokine receptor subunit (an interleukin receptor subunit) is fused to
CC   human kappa light chain (See GENESEQ record AAA54474). The two sequences
CC   are fused together using two primers (AAA54475, AAA54476)
XX
SQ   Sequence 330 AA;

  Query Match             98.0%;  Score 1729;  DB 4;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 1.7e-122;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||:|:|||||||||||||||||||||| ||||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 3
AAM47856
ID   AAM47856 standard; protein; 330 AA.
XX
AC   AAM47856;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Human Ig-gamma1 heavy chain constant region amino acid sequence.
XX
KW   Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
KW   human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
KW   transgenic plant.
XX
```

Homo sapiens.

WO200183529-A2.

08-NOV-2001.

28-APR-2001; 2001WO-US013932.

28-APR-2000; 2000US-0200298P.

(PLAN-) PLANET BIOTECHNOLOGY INC.

Larrick JW, Wycoff KL;

WPI; 2002-041481/05.
N-PSDB; ABA05265.

Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory component in association.

Disclosure; Fig 7; 138pp; English.

The invention relates to an immunoadhesin comprising: (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain; and (b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and reduces its infectivity, competing with cell surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature release of viral RNA and formation of empty capsids. Expression of the immunoadhesin in plants would be tetrameric, rather than dimeric. Immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the mucosal environment. Production is significantly less expensive in plants than in animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a human immunoglobulin protein sequence, useful to the invention

Sequence 330 AA;

```
Query Match             98.0%;  Score 1729;  DB 5;  Length 330;
Best Local Similarity   97.9%;  Pred. No. 1.7e-122;
Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:||||||||||||||||||||||||| ||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

RESULT 4
AAE21960
ID AAE21960 standard; protein; 330 AA.
XX
AC AAE21960;
XX
DT 25-JUL-2002 (first entry)
XX
DE Human death domain containing receptor (DR6) protein-related protein.
XX
KW Human; therapy; death domain containing receptor; DR6; receptor; anaemia;
KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;
KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;
KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;
KW autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;
KW H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide;
KW acquired immunedeficiency syndrome; AIDS; human immunodeficiency virus;
KW HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective;
KW adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic;
KW dermatological; hepatotropic; antibacterial.
XX
OS Homo sapiens.
XX
PN WO200185209-A2.
XX
PD 15-NOV-2001.
XX
PF 30-APR-2001; 2001WO-US011735.
XX
PR 10-MAY-2000; 2000US-0203015P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Heuer JG, Liu J, Na S, Song HY, Yang D;
XX
DR WPI; 2002-351283/38.
XX
PT Treating or preventing T cell or Th2 cell mediated condition e.g., asthma
PT or multiple sclerosis in mammal, comprises administering composition
PT comprising death domain containing receptor, DR6 agonist or antagonist.
XX
PS Disclosure; Page 132-133; 133pp; English.
XX
CC The invention relates to a method for treating or preventing a T cell
CC mediated condition or a Th2 cell mediated condition in a mammal. The
CC method comprising administering to the mammal a pharmaceutical
CC composition comprising a death domain containing receptor (DR6) agonist
CC or antagonist. The method is useful for treating or preventing a T cell
CC mediated condition or a Th2 cell mediated condition in a mammal. A DR6
CC agonist is useful in the manufacture of a medicament for treating or
CC preventing at least one symptom associated with aberrant apoptosis, graft
CC -versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma, atopy,
CC inflammatory bowel disease, vasculitis, psoriasis, pancreatitis, insulin-
CC dependent diabetes mellitus, cancer, multiple sclerosis, Hashimoto's
CC thyroiditis, Graves disease, transplant rejection, systemic lupus
CC erythematosus, autoimmune dermatosis, autoimmune cardiopathy, autoimmune
CC infertility, Behcet's disease, autoimmune gastritis, fibrosing lung
CC disease, organ rejection after transplantation, thrombotic
CC thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic
CC uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ
CC dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS)
CC or a condition or symptom related to the above mentioned diseases in a
CC mammal. An DR6 antagonist is useful in the manufacture of a medicament
CC for treating or preventing at least one symptom associated with
CC immunodeficiency, aberrant apoptosis, bacterial, viral or microbial
CC infection, complications of infection, human immunodeficiency virus
CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunedeficiency
CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis
CC C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori
CC associated ulceration, cytoprotection during cancer treatment,

```
CC   recuperation from chemotherapy, recuperation from irradiation therapy, or
CC   a condition or symptom related to the above mentioned diseases in a
CC   mammal. The present sequence is human DR6 protein-related protein
XX
SQ   Sequence 330 AA;

  Query Match             98.0%;  Score 1729;  DB 5;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 1.7e-122;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 5
ABB81641
ID   ABB81641 standard; protein; 330 AA.
XX
AC   ABB81641;
XX
DT   25-SEP-2002  (first entry)
XX
DE   Human IgG gamma 1 heavy chain SEQ ID NO:15.
XX
KW   Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;
KW   antirheumatic; antiarthritic; neuroprotective; antiinflammatory;
KW   antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic;
KW   vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus;
KW   autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;
KW   diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;
KW   immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;
KW   mesangioproliferative disease; chronic lymphocytic leukaemia; bronchitis;
KW   secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;
KW   haemolytic uraemic syndrome; renal neoplasm; urological neoplasm;
KW   emphysema; chronic airway disease.
XX
OS   Homo sapiens.
XX
PN   WO200244209-A2.
XX
PD   06-JUN-2002.
XX
PF   28-NOV-2001; 2001WO-US044808.
XX
PR   28-NOV-2000; 2000US-0253561P.
PR   07-FEB-2001; 2001US-0267211P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Xu W,  Novak JE,  Whitmore TE,  Grant FJ;
XX
DR   WPI; 2002-527700/56.
DR   N-PSDB; ABQ73076.
XX
PT   Novel Zyctor19 polypeptides and polynucleotides useful for stimulating
PT   immune responses in animals for producing antibodies, and for treating
PT   autoimmune diseases, leukemia and asthma.
XX
PS   Example 7; Page 171-172; 200pp; English.
XX
CC   The present invention describes an isolated human zcytor19 protein (I),
CC   and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,
CC   antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC   antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic
CC   activities, and can be used in vaccines. (I) or an antibody binding (I)
CC   can be used for suppressing the immune system for reducing rejection of
CC   tissue or organ transplants and grafts and for treating T-cell specific
CC   leukaemias or lymphomas and autoimmune diseases including rheumatoid
CC   arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel
CC   disease and Crohn's disease. The antibodies can also be used for treating
CC   immunologic renal diseases, glomerulonephritis, mesangioproliferative
CC   disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or
CC   vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related
CC   diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the
CC   antibodies can also be used for renal or urological neoplasms and
CC   multiple myelomas, asthma, bronchitis, emphysema and other chronic airway
CC   diseases. Human zcytor19 is located to chromosome 1, more specifically to
CC   chromosome 1p36.11. The present sequence represents a human IgG gamma 1
CC   heavy chain protein, which is used in an example from the present
CC   invention
XX
SQ   Sequence 330 AA;

  Query Match             98.0%;  Score 1729;  DB 5;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 1.7e-122;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 6
ABB05736
ID   ABB05736 standard; protein; 330 AA.
XX
AC   ABB05736;
XX
DT   01-MAY-2002  (first entry)
XX
DE   Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.
XX
KW   Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW   antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
KW   muscular; lymphoid; immune; inflammatory; spleenic; blood; bone;
```

infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.

Homo sapiens.

WO200200721-A2.

03-JAN-2002.

26-JUN-2001; 2001WO-US020484.

26-JUN-2000; 2000US-0214282P.
29-JUN-2000; 2000US-0214955P.
08-FEB-2001; 2001US-0267963P.

(ZYMO-) ZYMOGENETICS INC.

Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL; Maurer MF;

WPI; 2002-090519/12.
N-PSDB; ABA93797.

Isolated polynucleotide encoding a cytokine receptor zyctor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders.

Example 17; Page 187-188; 235pp; English.

The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the exemplification of the present invention

Sequence 330 AA;

```
Query Match             98.0%;  Score 1729;  DB 5;  Length 330;
Best Local Similarity   97.9%;  Pred. No. 1.7e-122;
Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

RESULT 7
ABP71856
ID ABP71856 standard; protein; 330 AA.
XX
AC ABP71856;
XX
DT 17-APR-2003 (first entry)
XX
DE Human IgG1 Fcgamma region.
XX
KW Human; fusion protein; IgE Fcepsilon; IgG Fcgamma; FcepsilonRI; allergy; KW FcepsilonRII; FcgammaRIIB; protein therapy; IgE; IgG; asthma; hay fever; KW allergic asthma; allergic rhinitis; hay fever; food allergy; KW atopic dermatitis; drug allergy; peanut allergen.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Region	1. .98
FT		/label= CH1 region
FT	Region	99. .113
FT		/label= Hinge_region
FT	Region	114. .223
FT		/label= CH2_region
FT	Region	224. .330
FT		/label= CH3_region

XX
PN WO2002102320-A2.
XX
PD 27-DEC-2002.
XX
PF 14-JUN-2002; 2002WO-US019448.
XX
PR 15-JUN-2001; 2001US-0298710P.
XX
PA (TANO-) TANOX INC.
XX
PI An L, Wu H, Fung MSC;
XX
DR WPI; 2003-167440/16.
XX
PT New fusion protein which binds to FcepsilonRI or RII receptor and PT FcgammaRIIB receptor, useful for treating or preventing allergies and PT asthma, comprises an IgE Fcepsilon fragment and an IgG Fcgamma fragment.
XX
PS Disclosure; Fig 5; 32pp; English.
XX
CC The invention relates to a novel fusion protein comprising an IgE CC Fcepsilon fragment and an IgG Fcgamma fragment, which binds to an CC FcepsilonRI and/or FcepsilonRII receptor and an FcgammaRIIB receptor. The CC fusion protein of the invention may have a use in protein therapy. The CC fusion protein is useful in treating or preventing IgE-mediated allergies CC and asthma, such as allergic asthma, allergic rhinitis, hay fever, food CC allergy, atopic dermatitis and drug allergy. The allergic response is CC particularly caused by peanut allergen. The present sequence represents CC the human IgG1 Fcgamma fragment
XX
SQ Sequence 330 AA;

```
  Query Match             98.0%;  Score 1729;  DB 6;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 1.7e-122;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
                 |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
                 ||||||||||||||:|:|||||||||||||||||||||||||| ||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
                 |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
                 |||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

RESULT 8
AAE32915
ID AAE32915 standard; protein; 330 AA.
XX
AC AAE32915;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.
XX
KW T-cell; immunogenic; therapy; human; immunoglobulin G1; IgG1.
XX
OS Homo sapiens.
XX
PN WO200279232-A2.
XX
PD 10-OCT-2002.
XX
PF 30-MAR-2002; 2002WO-US009815.
XX
PR 30-MAR-2001; 2001US-0280625P.
XX
PA (LEXI-) LEXIGEN PHARM CORP.
XX
PI Gillies SD;
XX
DR WPI; 2003-103259/09.
XX
PT Reducing the immunogenicity of a fusion protein comprises changing an
PT amino acid within the junction region to reduce the ability of the
PT candidate T-cell epitope identified within the junction spanning to
PT interact with T-cell receptor.
XX
PS Disclosure; Page 49-50; 68pp; English.
XX
CC The invention relates to a method for reducing the immunogenicity of a
CC fusion protein which involves identifying a candidate T-cell epitope
CC within a junction spanning a fusion junction of a fusion protein, and
CC changing an amino acid within the junction region to reduce the ability
CC of the candidate T-cell epitope to interact with a T-cell receptor. The
CC method is useful for reducing the immunogenicity of a fusion protein. It
CC is useful for analysing, changing or modifying one or more amino acids in
CC the junction region of a fusion protein to identify a T-cell epitope and
CC reduce its ability to interact with a T-cell receptor. The less
CC immunogenic fusion proteins are useful in providing therapeutic
CC treatment. The present sequence is human immunoglobulin G1 (IgG1) heavy
CC chain Fc region used to illustrate the method of the invention
XX
SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 1.7e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||:|:|||||||||||||||||||||||||| ||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

RESULT 9
AAE32627
ID AAE32627 standard; protein; 330 AA.
XX
AC AAE32627;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.
XX
KW Human; immunogenic; therapy; immunoglobulin G1; IgG1.
XX
OS Homo sapiens.
XX
PN WO200279415-A2.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009650.
XX
PR 30-MAR-2001; 2001US-0280625P.
XX
PA (LEXI-) LEXIGEN PHARM CORP.
XX
PI Gillies SD;
XX
DR WPI; 2003-111794/10.
XX
PT Reducing the immunogenicity of a fusion protein by changing an amino acid
PT within the junction region spanning a fusion junction of a fusion protein
PT to reduce the ability of the candidate T-cell epitope to interact with a
PT T-cell receptor.
XX
PS Disclosure; Page 49-50; 67pp; English.
XX
CC The present invention relates to a method of reducing the immunogenicity
CC of a fusion protein. The method involves identifying a candidate T-cell
CC epitope within a junction region spanning a fusion junction of a fusion
CC protein and changing an amino acid within the junction region to reduce
CC the ability of the candidate T-cell epitope to interact with a T-cell
CC receptor. The method is useful for reducing the immunogenicity of fusion
CC proteins for use in therapy. The present sequence is human immunoglobulin
CC G1 (IgG1) heavy chain Fc region. This sequence is used to illustrate the
CC method of the invention
XX
SQ Sequence 330 AA;

```
Query Match           98.0%;  Score 1729;  DB 6;  Length 330;
Best Local Similarity  97.9%;  Pred. No. 1.7e-122;
Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
            |||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||||
        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
            |||||||||||||||||||| |:||||||||
        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

```
SULT 10
BR82103
ID   ABR82103 standard; protein; 330 AA.

XX
AC   ABR82103;

XX
DT   23-SEP-2003  (first entry)

XX
DE   Human DR6 related amino acid sequence SEQ ID NO:5.

XX
KW   Human; DR6; B-cell mediated disease; immunosuppressive; antirheumatic;
KW   antiarthritic; antiasthmatic; dermatological; antiinflammatory;
KW   antipsoriatic; antidiabetic; cytostatic; neuroprotective; thyromimetic;
KW   antithyroid; nephrotropic; antiinfertility; vasotropic; virucide;
KW   hepatotropic; antibacterial; antiulcer; haemostatic; antianaemic;
KW   antimicrobial; anti-HIV; DR6 agonist; DR6 antagonist; immunity.

XX
OS   Homo sapiens.

XX
PN   WO2003051290-A2.

XX
PD   26-JUN-2003.

XX
PF   10-DEC-2002; 2002WO-US037596.

XX
PR   17-DEC-2001; 2001US-0342632P.

XX
PA   (ELIL ) LILLY & CO ELI.

XX
PI   Liu J,  Na S,  Song HY,  Yang D;

XX
DR   WPI; 2003-541604/51.

XX
PT   Treating or preventing a B cell mediated condition e.g., chronic
PT   hepatitis or chronic cirrhosis, in a mammal by administering a
PT   pharmaceutical composition comprising a DR6 agonist or DR6 antagonist to
PT   the mammal.

XX
PS   Disclosure; Page 96-97; 97pp; English.

XX
CC   The present invention describes a method (M1) for treating or preventing
CC   a B cell mediated condition in a mammal by administering a pharmaceutical
CC   composition comprising a DR6 agonist or DR6 antagonist to the mammal.
CC   Also described: (1) inhibiting B cell mediated immunity in a mammal, by
CC   administering a pharmaceutical composition comprising at least one DR6
CC   agonist; (2) use of a DR6 agonist in the manufacture of a medicament for
CC   treating or preventing at least one symptom associated with conditions
CC   (C1) such as aberrant apoptosis, graft-versus-host disease (GVHD), atopy,
CC   rheumatoid arthritis, asthma, eczema, inflammatory bowel disease, cancer,
CC   vasculitis, psoriasis, insulin-dependent diabetes mellitus, pancreatitis,
CC   psoriasis, multiple sclerosis, Hashimoto's thyroiditis, Graves' disease,
CC   transplant rejection, systemic lupus erythematosus, Behcet's disease,
CC   autoimmune nephropathy, autoimmune haematopathy, idiopathic interstitial
CC   pneumonia, hypersensitivity pneumonitis, autoimmune dermatosis,
CC   autoimmune cardiopathy, autoimmune infertility, autoimmune gastritis,
CC   fibrosing lung disease, fulminant viral hepatitis B, fulminant viral
CC   hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis,
CC   Helicobacter pylori-associated ulceration, organ rejection after
CC   transplantation, chronic glomerulonephritis, thrombotic thrombocytopenic
CC   purpura (TTP) and haemolytic uraemic syndrome (HUS), aplastic anaemia,
CC   myelodysplasia, multiple organ dysfunction syndrome (MDS), adult
CC   respiratory distress syndrome (ARDS), and at least one condition or
CC   symptom related to the conditions, in a mammal; and (3) use of DR6
CC   antagonist in the manufacture of a medicament for treating or preventing
CC   at least one symptom associated with conditions (C2) such as aberrant
CC   apoptosis, immunodeficiency, bacterial infection, viral infection,
CC   microbial infection, complications of infection, HIV, HIV-induced
CC   lymphoma, HIV-induced AIDS, fulminant viral hepatitis B, fulminant viral
CC   hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis,
CC   H. pylori-associated ulceration, cytoprotection during cancer treatment,
CC   recuperation from chemotherapy, recuperation from irradiation therapy,
CC   and at least one condition or symptom related to the conditions, in a
CC   mammal. DR6 has immunosuppressive, antirheumatic, antiarthritic,
CC   antiasthmatic, dermatological, antiinflammatory, antipsoriatic,
CC   antidiabetic, cytostatic, neuroprotective, thyromimetic, antithyroid,
CC   nephrotropic, antiinfertility, vasotropic, virucide, hepatotropic,
CC   antibacterial, antiulcer, haemostatic, antianaemic, antimicrobial and
CC   anti-HIV activities. (M1) is useful for treating or preventing at least
CC   one symptom associated with (C1) in a mammal, preferably human, by
CC   administering DR6 agonist, and for treating or preventing at least one
CC   symptom associated with (C2) by administering DR6 antagonist. The present
CC   sequence represents a human DR6 related amino acid sequence, which is
CC   given in the exemplification of the present invention
XX
SQ   Sequence 330 AA;
```

```
  Query Match           98.0%;  Score 1729;  DB 6;  Length 330;
  Best Local Similarity  97.9%;  Pred. No. 1.7e-122;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||||||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

```
RESULT 11
AAO31102
```

```
ID   AAO31102 standard; protein; 330 AA.
XX
AC   AAO31102;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human A2-G8 SCF antibody heavy chain constant region.
XX
KW   Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;
KW   steel factor; c-kit ligand; gene therapy; heavy chain.
XX
OS   Homo sapiens.
XX
PN   WO2003051311-A2.
XX
PD   26-JUN-2003.
XX
PF   16-DEC-2002; 2002WO-US040227.
XX
PR   17-DEC-2001; 2001US-0342174P.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Takeuchi T,  Tomkinson A,  Neben S;
XX
DR   WPI; 2003-523500/49.
DR   N-PSDB; AAL62618.
XX
PT   New purified human antibody that binds to stem cell factor protein,
PT   useful for preparing a composition for treating asthma.
XX
PS   Example 10; Page 47-48; 94pp; English.
XX
CC   The invention provides human antibodies that bind to stem cell factor
CC   (SCF) protein. SCF is also known as mast cell growth factor, steel factor
CC   or c-kit ligand. Antibodies of the invention are useful for preparing
CC   compositions for treating asthma. They are also used in gene therapy. The
CC   present sequence is human SCF antibody heavy chain constant region
XX
SQ   Sequence 330 AA;

  Query Match             98.0%;  Score 1729;  DB 6;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 1.7e-122;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||| ||||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 12
ABR55836
ID   ABR55836 standard; protein; 330 AA.
XX
AC   ABR55836;
XX
DT   02-SEP-2003  (first entry)
XX
DE   Anti-Ang-2 antibody IgG1 constant region.
XX
KW   Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic;
KW   gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
KW   angiogenesis; antibody; human.
XX
OS   Homo sapiens.
XX
PN   WO2003030833-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032613.
XX
PR   11-OCT-2001; 2001US-0328604P.
PR   10-OCT-2002; 2002US-00269805.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Oliner JD;
XX
DR   WPI; 2003-504963/47.
XX
PT   New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful
PT   for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
PT   hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX
PS   Example 4; Page 96; 161pp; English.
XX
CC   The invention relates to a specific binding agent, which comprises at
CC   least one peptide selected from any of 62 peptides (ABR55769-830) or its
CC   fragment. The binding agents are antibodies that recognize and bind to
CC   angiopoietin-2 (Ang-2). The specific binding agent, particularly the
CC   antibody, is useful for inhibiting undesired angiogenesis, treating
CC   cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
CC   2 activity, modulating vascular permeability or plasma leakage, or
CC   treating a disease (e.g. ocular neovascular disease, obesity,
CC   haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
CC   inflammatory disorders, atherosclerosis, endometriosis, neoplastic
CC   disease, bone-related disease, or psoriasis) in a mammal. The present
CC   sequence represents a human IgG1 constant region of an anti-Ang-2
CC   antibody
XX
SQ   Sequence 330 AA;

  Query Match             98.0%;  Score 1729;  DB 6;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 1.7e-122;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||| ||||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
```

```
Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              ||||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

SULT 13
AO30893
AAO30893 standard; protein; 330 AA.

AAO30893;

22-SEP-2003 (first entry)

Human immunoglobulin gamma (IgG) 1 constant region.

Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder; gene therapy; immunoglobulin; Ig; human.

Homo sapiens.

WO2003048334-A2.

12-JUN-2003.

04-DEC-2002; 2002WO-US038780.

04-DEC-2001; 2001US-0337113P.
12-APR-2002; 2002US-0371966P.

(EMDL-) EMD LEXIGEN RES CENT CORP.

Gillies SD;

WPI; 2003-513757/48.

New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2 moiety, useful for preparing a composition for treating cancer, viral infections or immune disorders.

Example 1; Page 51-53; 71pp; English.

The invention relates to cytokine fusion proteins with increased therapeutic index and methods for increasing the therapeutic index of such fusion proteins. The fusion protein comprises a non-interleukin-2 (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a composition for treating cancer, viral infections or immune disorders. The fusion protein is also used in gene therapy. The present sequence is human immunoglobulin gamma (IgG) constant region. This sequence is used to illustrate the method of the invention

Sequence 330 AA;

```
Query Match             98.0%;  Score 1729;  DB 6;  Length 330;
Best Local Similarity   97.9%;  Pred. No. 1.7e-122;
Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              ||||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

RESULT 14
ADF11389
ID ADF11389 standard; protein; 330 AA.
XX
AC ADF11389;
XX
DT 12-FEB-2004 (first entry)
XX
DE Anti-OPGL antibody heavy chain constant region SEQ ID NO:2.
XX
KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX
OS Homo sapiens.
XX
PN WO2003086289-A2.
XX
PD 23-OCT-2003.
XX
PF 07-APR-2003; 2003WO-US010749.
XX
PR 05-APR-2002; 2002US-0370407P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
XX
DR WPI; 2003-845253/78.
DR N-PSDB; ADF11388.
XX
PT New isolated antibody that specifically binds osteoprotegerin ligand,
PT useful for diagnosing or treating bone disorders, such as osteoporosis,
PT bone loss from arthritis, Paget's disease or osteopenia.
XX
PS Example 3; SEQ ID NO 2; 156pp; English.
XX
CC The present invention describes an isolated human antibody (I) that
CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
CC pharmaceutical composition comprising a pharmaceutical carrier and a
CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
CC in a patient, comprising administering to a patient the pharmaceutical
CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
CC for detecting OPGL in a biological sample, comprising contacting the
CC sample with (I) under conditions that allow for binding of the antibody
CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
CC osteopathic, antiarthritic and cytostatic activities, and can be used in
CC gene therapy. The composition and methods are useful in diagnosing or
CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
CC Paget's disease or osteopenia. The antibody (I) may also be used for
CC detecting OPGL in biological samples and in identifying cells or tissues
CC that produce the protein. The present sequence represents a sequence
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 330 AA;

```
  Query Match             98.0%;  Score 1729;  DB 7;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 1.7e-122;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
```

```
Qy          61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy         121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy         181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
               |||||||||||||:|:|||||||||||||||||||||||||| ||||||||||||||||
Db         181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy         241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
               |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy         301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
               |||||||||||||||||| |:||||||||
Db         301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
```

RESULT 15
ADE97351
ID ADE97351 standard; protein; 330 AA.
XX
AC ADE97351;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human IgG1 heavy chain constant region protein - SEQ ID 20.
XX
KW immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;
KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;
KW intercellular adhesion molecule; ICAM-1; human; constant region; IgG.
XX
OS Homo sapiens.
XX
PN WO2003064992-A2.
XX
PD 07-AUG-2003.
XX
PF 25-OCT-2002; 2002WO-US034197.
XX
PR 26-OCT-2001; 2001US-00047542.
XX
PA (PLAN-) PLANET BIOTECHNOLOGY INC.
PA (LARR/) LARRICK J W.
PA (WYCO/) WYCOFF K L.
XX
PI Larrick JW, Wycoff KL;
XX
DR WPI; 2003-636816/60.
DR N-PSDB; ADE97350, ADE97376.
XX
PT New immunoadhesin, useful for treating anthrax and rhinovirus, comprises
PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and
PT J chain and secretory component associated with the chimeric toxin
PT receptor protein.
XX
PS Disclosure; SEQ ID NO 20; 288pp; English.
XX
CC The invention relates to a novel immunoadhesin comprising a chimeric
CC toxin receptor protein consisting of a toxin receptor protein linked to
CC at least a portion of an immunoglobulin heavy chain with a J (joining)
CC chain and secretory component (SC) associated with the chimeric toxin
CC receptor protein. The immunoadhesin comprises a chimeric bacterial or
CC viral toxin receptor protein and the immunoadhesin has plant-specific
CC glycosylation. The immunoadhesin of the invention demonstrates virucide
CC and antibacterial activities and may be useful for reducing the binding
CC of a viral or bacterial antigen to a host cell and thus for treating or
CC preventing anthrax, as well as human rhinovirus infection which results
CC in the common cold. The current sequence is that of the human
CC immunoadhesion-related protein of the invention.

XX
SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 1.7e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy           1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy          61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy         121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy         181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
               |||||||||||||:|:|||||||||||||||||||||||||| ||||||||||||||||
Db         181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy         241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
               |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy         301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
               |||||||||||||||||| |:||||||||
Db         301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1764	100.0	330	14	US-10-000-439-2	Sequence 2, Appli
3	1729	98.0	330	10	US-09-995-898A-15	Sequence 15, Appl
4	1729	98.0	330	10	US-09-892-949-38	Sequence 38, Appl
5	1729	98.0	330	13	US-10-047-542-20	Sequence 20, Appl
6	1729	98.0	330	14	US-10-269-805-68	Sequence 68, Appl
7	1729	98.0	330	14	US-10-310-719-8	Sequence 8, Appli
8	1729	98.0	330	14	US-10-112-582-1	Sequence 1, Appli
9	1729	98.0	330	14	US-10-320-231A-81	Sequence 81, Appl
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15	1729	98.0	330	16	US-10-772-531-38	Sequence 38, Appl
16	1729	98.0	330	17	US-10-479-326-1	Sequence 1, Appli
17	1729	98.0	332	10	US-09-990-586-98	Sequence 98, Appl
18	1729	98.0	332	14	US-10-310-113-167	Sequence 167, App
19	1729	98.0	332	14	US-10-230-880-98	Sequence 98, Appl
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21	1729	98.0	356	15	US-10-272-899A-72	Sequence 72, Appl
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33	1729	98.0	446	15	US-10-408-901-30	Sequence 30, Appl
34	1729	98.0	446	15	US-10-408-901-38	Sequence 38, Appl
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36	1729	98.0	446	15	US-10-408-901-50	Sequence 50, Appl
37	1729	98.0	446	15	US-10-435-299-7	Sequence 7, Appli
38	1729	98.0	447	10	US-09-256-156-1	Sequence 1, Appli
39	1729	98.0	448	15	US-10-378-567-2	Sequence 2, Appli
40	1729	98.0	451	9	US-09-822-698A-26	Sequence 26, Appl
41	1729	98.0	453	17	US-10-813-483-6	Sequence 6, Appli
42	1729	98.0	467	15	US-10-108-260A-4293	Sequence 4293, Ap
43	1729	98.0	467	15	US-10-656-769-32	Sequence 32, Appl
44	1729	98.0	469	15	US-10-656-769-20	Sequence 20, Appl
45	1729	98.0	469	15	US-10-656-769-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-847-208-2
; Sequence 2, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IgE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-2

Query Match 100.0%; Score 1764; DB 10; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
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Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||||||||||||||
Db        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330


RESULT 2
US-10-000-439-2
; Sequence 2, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
;  APPLICANT: Saxon, Andrew
;  TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
;  TITLE OF INVENTION:  TREATMENT OF IMMUNE DISEASES
;  FILE REFERENCE: UC067.004A
;  CURRENT APPLICATION NUMBER: US/10/000,439
;  CURRENT FILING DATE:  2001-10-24
;  PRIOR APPLICATION NUMBER: US 09/847,208
;  PRIOR FILING DATE: 2001-05-01
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-000-439-2

  Query Match             100.0%;  Score 1764;  DB 14;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-128;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||||||||||||||
Db        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330


RESULT 3
US-09-995-898A-15
; Sequence 15, Application US/09995898A
; Publication No. US20030027253A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  No. US20030027253A1ak, Julia E.
;  APPLICANT:  Whitmore, Theodore E.
;  APPLICANT:  Grant, Francis J.
;  TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
;  FILE REFERENCE: 00-108
;  CURRENT APPLICATION NUMBER: US/09/995,898A
;  CURRENT FILING DATE:  2001-11-28
;  PRIOR APPLICATION NUMBER: US 60/253,561
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: US 60/267,211
;  PRIOR FILING DATE: 2001-02-07
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-995-898A-15

  Query Match             98.0%;  Score 1729;  DB 10;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 6.4e-126;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||:|:|||||||||||||||||||||||||| ||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 4
US-09-892-949-38
; Sequence 38, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
;  APPLICANT: Sprecher, Cindy A.
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Gao, Zeren
;  APPLICANT:  Whitmore, Theodore E.
;  APPLICANT:  Kuijper, Joseph L.
;  APPLICANT:  Maurer, Mark F.
;  TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
;  FILE REFERENCE: 00-42
;  CURRENT APPLICATION NUMBER: US/09/892,949
;  CURRENT FILING DATE:  2001-06-26
;  PRIOR APPLICATION NUMBER: US 60/214,282
;  PRIOR FILING DATE: 2000-06-26
;  PRIOR APPLICATION NUMBER: US 60/214,955
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: US 60/267,963
;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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-09-892-949-38

Query Match 98.0%; Score 1729; DB 10; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
            |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
            |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||
        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
            |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
            |||||||||||||||||||| |:||||||||
        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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:SULT 5
;-10-047-542-20
Sequence 20, Application US/10047542
Publication No. US20020168367A1
GENERAL INFORMATION:
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
S-10-047-542-20

Query Match 98.0%; Score 1729; DB 13; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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y           1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b           1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

y          61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

y         121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
b         121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

y         181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||
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```
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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RESULT 6
US-10-269-805-68
; Sequence 68, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-68

Query Match 98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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RESULT 7
US-10-310-719-8
; Sequence 8, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966

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;  PRIOR FILING DATE: 2002-04-12
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc
;   LOCATION: (1)..(330)
;   OTHER INFORMATION: IgG1 constant region
US-10-310-719-8

  Query Match             98.0%;  Score 1729;  DB 14;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 6.4e-126;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 8
US-10-112-582-1
; Sequence 1, Application US/10112582
; Publication No. US20030166877A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
;  FILE REFERENCE: LEX-017
;  CURRENT APPLICATION NUMBER: US/10/112,582
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/280,625
;  PRIOR FILING DATE: 2001-03-30
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1

  Query Match             98.0%;  Score 1729;  DB 14;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 6.4e-126;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 9
US-10-320-231A-81
; Sequence 81, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
;  APPLICANT: Neben, Steven
;  APPLICANT:  Takeuchi, Toshihiko
;  APPLICANT:  Tomkinson, Adrian
;  TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
;  TITLE OF INVENTION:  Treatment Of Asthma
;  FILE REFERENCE: 7430*163
;  CURRENT APPLICATION NUMBER: US/10/320,231A
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/342,174
;  PRIOR FILING DATE: 2001-12-17
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-320-231A-81

  Query Match             98.0%;  Score 1729;  DB 14;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 6.4e-126;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
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Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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SULT 10
-10-383-902A-6
Sequence 6, Application US/10383902A
Publication No. US20030224408A1
GENERAL INFORMATION:
 APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
 APPLICANT:  Mullberg, Jurgen
 APPLICANT:  Ladner, Robert C.
 TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY
 FILE REFERENCE: 10280-042001
 CURRENT APPLICATION NUMBER: US/10/383,902A
 CURRENT FILING DATE:  2003-03-07
 PRIOR APPLICATION NUMBER: US 60/362,403
 PRIOR FILING DATE: 2002-03-07
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
  LENGTH: 330
  TYPE: PRT
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: synthetically generated plasmid sequence
-10-383-902A-6

Query Match             98.0%;  Score 1729;  DB 14;  Length 330;
Best Local Similarity   97.9%;  Pred. No. 6.4e-126;
Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
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Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
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Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


ESULT 11
3-10-408-901-2
 Sequence 2, Application US/10408901
 Publication No. US20040023313A1
 GENERAL INFORMATION:
  APPLICANT: Boyle, William
  APPLICANT:  Huang, Haichun
  APPLICANT:  Elliot, Robin
  APPLICANT:  Sullivan, John
  APPLICANT:  Medlock, Eugene
  APPLICANT:  Martin, Francis
  TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
  TITLE OF INVENTION:  Inhibitors
  FILE REFERENCE: MBHB 01-1145-A
  CURRENT APPLICATION NUMBER: US/10/408,901
  CURRENT FILING DATE:  2003-04-07
  NUMBER OF SEQ ID NOS: 76
  SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2
   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-901-2

  Query Match             98.0%;  Score 1729;  DB 15;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 6.4e-126;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 12
US-10-420-034A-15
; Sequence 15, Application US/10420034A
; Publication No. US20040029228A1
; GENERAL INFORMATION:
;  APPLICANT: Presnell, Scott R.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  No. US20040029228A1ak, Julia E.
;  APPLICANT:  Whitmore, Theodore E.
;  APPLICANT:  Grant, Francis J.
;  APPLICANT:  Kindsvogel, Wayne R.
;  APPLICANT:  Klucher, Kevin M.
;  TITLE OF INVENTION: CYTOKINE RECEPTOR
;  FILE REFERENCE: 02-10
;  CURRENT APPLICATION NUMBER: US/10/420,034A
;  CURRENT FILING DATE:  2003-04-18
;  PRIOR APPLICATION NUMBER: 60/373,813
;  PRIOR FILING DATE: 2002-04-19
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-420-034A-15

  Query Match             98.0%;  Score 1729;  DB 15;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 6.4e-126;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
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Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||:|:||||||||||||||||||||||||||| ||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 13
US-10-257-907-5
; Sequence 5, Application US/10257907
; Publication No. US20040043022A1
; GENERAL INFORMATION:
;  APPLICANT: Heuer, Josef
;  APPLICANT:  Liu, Jinqi
;  APPLICANT:  Na, Songqing
;  APPLICANT:  Song, Ho Yeong
;  APPLICANT:  Yang, Derek Di
;  TITLE OF INVENTION: TREATING T-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY
;  FILE REFERENCE: X-13992
;  CURRENT APPLICATION NUMBER: US/10/257,907
;  CURRENT FILING DATE:  2002-10-16
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-257-907-5

  Query Match           98.0%;  Score 1729;  DB 15;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 6.4e-126;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
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Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
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Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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RESULT 14
US-10-656-769-2
; Sequence 2, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
;  APPLICANT: Varnum, Brian
;  APPLICANT:  Witte, Alison
;  APPLICANT:  Vezina, Chris
;  APPLICANT:  Wong, Lu Min
;  APPLICANT:  Qian, Xueming
;  TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
;  FILE REFERENCE: 01,1554
;  CURRENT APPLICATION NUMBER: US/10/656,769
;  CURRENT FILING DATE:  2003-09-05
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-656-769-2

  Query Match           98.0%;  Score 1729;  DB 15;  Length 330;
  Best Local Similarity   97.9%;  Pred. No. 6.4e-126;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||:|:||||||||||||||||||||||||||| ||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
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Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 15
US-10-772-531-38
; Sequence 38, Application US/10772531
; Publication No. US20040142422A1
; GENERAL INFORMATION:
;  APPLICANT: Sprecher, Cindy A.
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Gao, Zeren
;  APPLICANT:  Whitmore, Theodore E.
;  APPLICANT:  Kuijper, Joseph L.
;  APPLICANT:  Maurer, Mark F.
;  TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
;  FILE REFERENCE: 00-42
;  CURRENT APPLICATION NUMBER: US/10/772,531
;  CURRENT FILING DATE:  2004-02-05
;  PRIOR APPLICATION NUMBER: US/09/892,949
;  PRIOR FILING DATE: 2001-06-26
;  PRIOR APPLICATION NUMBER: US 60/214,282
;  PRIOR FILING DATE: 2000-06-26
;  PRIOR APPLICATION NUMBER: US 60/214,955
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: US 60/267,963
;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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-10-772-531-38

Query Match 98.0%; Score 1729; DB 16; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
            |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
            |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
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        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
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        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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b time : 102.996 secs

GenCore version 5.1.6

protein - protein search, using sw model

n on: October 27, 2004, 16:51:34 ; Search time 32.8826 Seconds
(without alignments)
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rfect score: 1764
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tal number of hits satisfying chosen parameters: 478139

nimum DB seq length: 0
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st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	1729	98.0	371	1	US-08-236-311-7	Sequence 7, Appli
2	1729	98.0	371	3	US-08-457-918-7	Sequence 7, Appli
3	1729	98.0	371	4	US-10-157-408-7	Sequence 7, Appli
4	1729	98.0	446	3	US-08-397-411-7	Sequence 7, Appli
5	1729	98.0	449	1	US-08-458-516-13	Sequence 13, Appl
6	1729	98.0	467	4	US-08-030-175-41	Sequence 41, Appl
7	1729	98.0	467	4	US-08-030-175-42	Sequence 42, Appl
8	1729	98.0	476	2	US-08-378-939-10	Sequence 10, Appl
9	1729	98.0	547	4	US-09-746-359A-54	Sequence 54, Appl
10	1729	98.0	567	4	US-09-825-561A-16	Sequence 16, Appl
11	1729	98.0	571	4	US-09-746-359A-53	Sequence 53, Appl
12	1729	98.0	951	4	US-09-313-942-9	Sequence 9, Appli
13	1725	97.8	462	4	US-09-289-942A-7	Sequence 7, Appli
14	1725	97.8	475	4	US-09-740-002-27	Sequence 27, Appl
15	1725	97.8	476	3	US-08-487-550-4	Sequence 4, Appli
16	1725	97.8	476	3	US-08-487-550-12	Sequence 12, Appl
17	1725	97.8	476	4	US-09-526-098-4	Sequence 4, Appli
18	1725	97.8	476	4	US-09-526-098-12	Sequence 12, Appl
19	1725	97.8	476	4	US-09-383-916-4	Sequence 4, Appli
20	1725	97.8	476	4	US-09-383-916-12	Sequence 12, Appl
21	1725	97.8	478	3	US-08-487-550-8	Sequence 8, Appli
22	1725	97.8	478	4	US-09-526-098-8	Sequence 8, Appli
23	1725	97.8	478	4	US-09-383-916-8	Sequence 8, Appli
24	1724	97.7	459	1	US-08-157-101A-7	Sequence 7, Appli
25	1724	97.7	475	4	US-09-740-002-25	Sequence 25, Appl
26	1723	97.7	330	4	US-09-301-593-22	Sequence 22, Appl
27	1723	97.7	451	2	US-08-887-352B-14	Sequence 14, Appl
28	1723	97.7	451	2	US-08-887-352B-16	Sequence 16, Appl
29	1723	97.7	451	2	US-08-887-352B-18	Sequence 18, Appl
30	1723	97.7	451	3	US-08-466-151-65	Sequence 65, Appl
31	1723	97.7	451	3	US-09-109-207C-14	Sequence 14, Appl
32	1723	97.7	451	3	US-09-109-207C-16	Sequence 16, Appl
33	1723	97.7	451	3	US-09-109-207C-18	Sequence 18, Appl
34	1723	97.7	451	3	US-09-282-505-2	Sequence 2, Appli
35	1723	97.7	451	3	US-09-054-255-2	Sequence 2, Appli
36	1723	97.7	451	3	US-09-296-005-14	Sequence 14, Appl
37	1723	97.7	451	3	US-09-296-005-16	Sequence 16, Appl
38	1723	97.7	451	3	US-09-296-005-18	Sequence 18, Appl
39	1723	97.7	451	4	US-09-282-846-2	Sequence 2, Appli
40	1723	97.7	451	4	US-09-680-145-2	Sequence 2, Appli
41	1723	97.7	451	4	US-09-920-171-14	Sequence 14, Appl
42	1723	97.7	451	4	US-09-920-171-16	Sequence 16, Appl
43	1723	97.7	451	4	US-09-920-171-18	Sequence 18, Appl
44	1723	97.7	451	4	US-09-716-028-14	Sequence 14, Appl
45	1723	97.7	451	4	US-09-716-028-16	Sequence 16, Appl

ALIGNMENTS

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RESULT 1
US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5565335
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/236,311
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  444P1C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  371 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
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US-08-236-311-7

Query Match 98.0%; Score 1729; DB 1; Length 371;
Best Local Similarity 97.9%; Pred. No. 3e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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Db         42 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 101

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 161

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        162 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||
Db        222 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 281

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 341

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        342 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371
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RESULT 2
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-457-918-7

Query Match 98.0%; Score 1729; DB 3; Length 371;
Best Local Similarity 97.9%; Pred. No. 3e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         42 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 101

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 161

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        162 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||
Db        222 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 281

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 341

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Db        342 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371
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RESULT 3
US-10-157-408-7
; Sequence 7, Application US/10157408
; Patent No. 6710169
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/157,408
; FILING DATE: 28-May-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 07/936190

FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
-10-157-408-7

Query Match 98.0%; Score 1729; DB 4; Length 371;
Best Local Similarity 97.9%; Pred. No. 3e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         42 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 101

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 161

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        162 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        222 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 281

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 341

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Db        342 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371
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ESULT 4
3-08-397-411-7
Sequence 7, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-7

Query Match 98.0%; Score 1729; DB 3; Length 446;
Best Local Similarity 97.9%; Pred. No. 3.9e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 236

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        237 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
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Db        297 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 356

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        357 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 416

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
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Db        417 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 446
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RESULT 5
US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:

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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,516
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/059,159
;      FILING DATE:  03-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-37-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  449 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-458-516-13

  Query Match             98.0%;  Score 1729;  DB 1;  Length 449;
  Best Local Similarity   97.9%;  Pred. No. 4e-157;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449


RESULT 6
US-08-030-175-41
; Sequence 41, Application US/08030175
; Patent No. 6767996
;  GENERAL INFORMATION:
;    APPLICANT:  Gorman, Scott D.
;    APPLICANT:  Clark, Michael R.
;    APPLICANT:  Cobbold, Stephen P.
;    APPLICANT:  Waldmann, Herman
;    TITLE OF INVENTION:  ALTERED ANTIBODIES AND THEIR PREPARATION
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rothwell, Figg, Ernst & Kurz, P. C.
;      STREET:  555 13TH ST., NW  Suite 701 East
;      CITY:  Washington
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk, 5.25 inch, 360 Kb storage
;      COMPUTER:  IBM AT compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS V 3.2
;      SOFTWARE:  WordPerfect 5.0 (Dos Text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/030,175
;      FILING DATE:  17-MAY-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB91/01578
;      FILING DATE:  13-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ernst, Barbara G.
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1768-113
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)783-6040
;      TELEFAX:  (202)783-6031
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-030-175-41

  Query Match             98.0%;  Score 1729;  DB 4;  Length 467;
  Best Local Similarity   97.9%;  Pred. No. 4.2e-157;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 257

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        258 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||||
Db        318 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 437

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        438 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 7
US-08-030-175-42
; Sequence 42, Application US/08030175
; Patent No. 6767996
;  GENERAL INFORMATION:
;    APPLICANT:  Gorman, Scott D.
;    APPLICANT:  Clark, Michael R.
;    APPLICANT:  Cobbold, Stephen P.
;    APPLICANT:  Waldmann, Herman
;    TITLE OF INVENTION:  ALTERED ANTIBODIES AND THEIR PREPARATION
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rothwell, Figg, Ernst & Kurz, P. C.
;      STREET:  555 13TH ST., NW  Suite 701 East
;      CITY:  Washington
;      STATE:  D. C.
```

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      COUNTRY:  U.S.
      ZIP:  20004
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk, 5.25 inch, 360 Kb storage
      COMPUTER:  IBM AT compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS V 3.2
      SOFTWARE:  WordPerfect 5.0 (Dos Text)
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/030,175
      FILING DATE:  17-MAY-1993
      CLASSIFICATION:  424
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  PCT/GB91/01578
      FILING DATE:  13-SEP-1991
    ATTORNEY/AGENT INFORMATION:
      NAME:  Ernst, Barbara G.
      REGISTRATION NUMBER:  30,377
      REFERENCE/DOCKET NUMBER:  1768-113
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  (202)783-6040
      TELEFAX:  (202)783-6031
  INFORMATION FOR SEQ ID NO:  42:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  467 amino acids
      TYPE:  amino acid
      TOPOLOGY:  linear
    MOLECULE TYPE:  protein
-08-030-175-42

Query Match             98.0%;  Score 1729;  DB 4;  Length 467;
Best Local Similarity   97.9%;  Pred. No. 4.2e-157;
Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        198 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 257

        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
            |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
        258 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317

        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
            |||||||||||||:|:|||||||||||||||||||||| ||||||||||||||||
        318 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377

        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
            |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
        378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 437

        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
            |||||||||||||||||| |:||||||||
        438 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467


SULT 8
-08-378-939-10
Sequence 10, Application US/08378939
Patent No. 5876961
 GENERAL INFORMATION:
   APPLICANT:  CROWE, JAMES SCOTT
   APPLICANT:  LEWIS, ALAN PETER
   TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
   NUMBER OF SEQUENCES:  46
   CORRESPONDENCE ADDRESS:
     ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
     STREET:  555 THIRTEENTH ST. N.W.
     CITY:  WASHINGTON
     STATE:  D. C.
     COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, BARBARA G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1808-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  476 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-939-10

  Query Match             98.0%;  Score 1729;  DB 2;  Length 476;
  Best Local Similarity   97.9%;  Pred. No. 4.3e-157;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 266

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:|||||||||||||||||||||| ||||||||||||||||
Db        327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476


RESULT 9
US-09-746-359A-54
; Sequence 54, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. 6610286ak, Julia E.
```

```
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 54
;   LENGTH: 547
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-54

  Query Match             98.0%;  Score 1729;  DB 4;  Length 547;
  Best Local Similarity   97.9%;  Pred. No. 5.3e-157;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 277

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 337

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        338 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 397

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:||||||||||||||||||||||||| ||||||||||||||||
Db        398 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 457

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        458 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 517

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        518 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 547


RESULT 10
US-09-825-561A-16
; Sequence 16, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
;  APPLICANT: Sprecher, Cindy A.
;  APPLICANT:  No. 6777539ak, Julia E.
;  APPLICANT:  West, James W.
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Holly, Richard D.
;  APPLICANT:  Nelson, Andrew J.
;  TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
;  FILE REFERENCE: 00-22
;  CURRENT APPLICATION NUMBER: US/09/825,561A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/194,731
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/222,121
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 567
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: soluble zalpha11R/IgGgamma1 polypeptide
US-09-825-561A-16

  Query Match             98.0%;  Score 1729;  DB 4;  Length 567;
  Best Local Similarity   97.9%;  Pred. No. 5.6e-157;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 297

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 357

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        358 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 417

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||:|:||||||||||||||||||||||||| ||||||||||||||||
Db        418 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 477

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        478 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 537

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        538 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 567


RESULT 11
US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. 6610286ak, Julia E.
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 53
;   LENGTH: 571
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-746-359A-53

  Query Match             98.0%;  Score 1729;  DB 4;  Length 571;
  Best Local Similarity   97.9%;  Pred. No. 5.7e-157;
  Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 301

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 361
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Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        362 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 421

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||||:|:|||||||||||||||||||||||||| ||||||||||||||||
Db        422 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 481

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        482 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 541

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        542 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 571


RESULT 12
US-09-313-942-9
 Sequence 9, Application US/09313942
 Patent No. 6472179
 GENERAL INFORMATION:
  APPLICANT: REGENERON PHARMACEUTICALS, INC.
  TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
  TITLE OF INVENTION:  AND USING
  FILE REFERENCE: REG 203-A
  CURRENT APPLICATION NUMBER: US/09/313,942
  CURRENT FILING DATE:  1999-05-19
  PRIOR APPLICATION NUMBER: 09/313,942
  PRIOR FILING DATE: 1999-05-19
  PRIOR APPLICATION NUMBER: 60/101,858
  PRIOR FILING DATE: 1998-09-25
  NUMBER OF SEQ ID NOS: 32
  SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 9
   LENGTH: 951
   TYPE: PRT
   ORGANISM: Homo sapiens
US-09-313-942-9

 Query Match            98.0%;  Score 1729;  DB 4;  Length 951;
 Best Local Similarity   97.9%;  Pred. No. 1.2e-156;
 Matches  323;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 681

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 741

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        742 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 801

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||||:|:|||||||||||||||||||||||||| ||||||||||||||||
Db        802 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 861

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        862 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 921

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        922 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 951


RESULT 13
US-09-289-942A-7
 Sequence 7, Application US/09289942A
 Patent No. 6482928
 GENERAL INFORMATION:
  APPLICANT: Pai, Emil F.
  APPLICANT:  Klein, Michel H.
  APPLICANT:  Chong, Pele
  APPLICANT:  Pedyczak, Arthur
  TITLE OF INVENTION: Fab'-EPITOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
  TITLE OF INVENTION:  MONOCLONAL ANTIBODY 2F5
  FILE REFERENCE: 1038-926 MIS:jb
  CURRENT APPLICATION NUMBER: US/09/289,942A
  CURRENT FILING DATE:  1999-04-13
  NUMBER OF SEQ ID NOS: 9
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
   LENGTH: 462
   TYPE: PRT
   ORGANISM: Human immunodeficiency virus type 1
US-09-289-942A-7

  Query Match            97.8%;  Score 1725;  DB 4;  Length 462;
  Best Local Similarity   97.6%;  Pred. No. 1e-156;
  Matches  322;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 192

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 252

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        253 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 312

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              |||||||||||||||:|:|||||||||||||||||||||||||| ||||||||||||||||
Db        313 STYRVVSVLTVLHQDWLNGKEYKCKVSNKAFPAPIEKTISKAKGQPREPQVYTLPPSRDE 372

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 432

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        433 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462


RESULT 14
US-09-740-002-27
 Sequence 27, Application US/09740002
 Patent No. 6537809
 GENERAL INFORMATION:
  APPLICANT: BRAMS, PETER
  APPLICANT:  MORROW, PHILLIP
  TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
  TITLE OF INVENTION:  SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
  TITLE OF INVENTION:  MANUFACTURE AND THERAPEUTIC USE THEREOF
  FILE REFERENCE: 037003-0275759
  CURRENT APPLICATION NUMBER: US/09/740,002
  CURRENT FILING DATE:  2000-12-20
  PRIOR APPLICATION NUMBER: 09/335,697
  PRIOR FILING DATE: 1999-06-18
  PRIOR APPLICATION NUMBER: 08/488,376
  PRIOR FILING DATE: 1995-06-07
  NUMBER OF SEQ ID NOS: 27
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 27
   LENGTH: 475
   TYPE: PRT
   ORGANISM: Homo sapiens
US-09-740-002-27
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  Query Match             97.8%;  Score 1725;  DB 4;  Length 475;
  Best Local Similarity   97.6%;  Pred. No. 1e-156;
  Matches  322;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 205

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        206 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 265

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        266 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 325

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||
Db        326 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 445

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        446 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475


RESULT 15
US-08-487-550-4
; Sequence 4, Application US/08487550
; Patent No. 6113898
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Darrell R.
;    TITLE OF INVENTION:  "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
;    TITLE OF INVENTION:  TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
;    TITLE OF INVENTION:  PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;    TITLE OF INVENTION:  IMMUNOSUPPRESANTS"
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,550
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-131
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 476 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-487-550-4

  Query Match             97.8%;  Score 1725;  DB 3;  Length 476;
  Best Local Similarity   97.6%;  Pred. No. 1e-156;
  Matches  322;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206

Qy         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        207 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG 266

Qy        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        267 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326

Qy        181 STYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
              ||||||||||||:|:|||||||||||||||||||||||| ||||||||||||||||
Db        327 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386

Qy        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRW 300
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 446

Qy        301 QQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330
              |||||||||||||||||| |:||||||||
Db        447 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476


Search completed: October 27, 2004, 17:05:52
Job time : 34.8826 secs
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GenCore version 5.1.6

4 protein - protein search, using sw model

Run on: October 27, 2004, 16:51:09 ; Search time 20.2278 Seconds
(without alignments)
1103.547 Million cell updates/sec

Title: US-10-000-439-3
Perfect score: 1260
Sequence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNHYQQRSLSLSPGK 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1225	97.2	330	1	GHHU	Ig gamma-1 chain C
2	1219	96.7	374	2	S69339	Ig heavy chain V r
3	1217	96.6	255	4	S31866	Ig gamma-1 chain C
4	1172	93.0	234	2	PT0207	Ig gamma chain C r
5	1138	90.3	377	2	A23511	Ig gamma-3 chain C
6	1136	90.2	377	2	A60764	Ig gamma-3 chain C
7	1123	89.1	289	1	G3HUWI	Ig gamma-3 heavy c
8	1107	87.9	326	1	G2HU	Ig gamma-2 chain C
9	1097	87.1	327	1	G4HU	Ig gamma-4 chain C
10	883	70.1	323	1	GHRB	Ig gamma chain C r
11	868.5	68.9	328	2	I47160	Ig gamma 2b chain
12	868.5	68.9	328	2	I47159	Ig gamma 2a chain
13	865	68.7	277	2	I47162	Ig gamma 4 chain c
14	858	68.1	329	1	G2GP	Ig gamma-2 chain C
15	847.5	67.3	328	2	I47158	Ig gamma 1 chain c
16	840.5	66.7	328	2	I47161	Ig gamma 3 chain c
17	820	65.1	470	2	S22080	Ig heavy chain pre
18	813	64.5	333	2	PS0018	Ig gamma-2b chain
19	812.5	64.5	329	1	G3MSC	Ig gamma-3 chain C
20	811.5	64.4	308	2	C30554	Ig heavy chain C r
21	811.5	64.4	472	2	S31459	Ig gamma-1 chain -
22	801.5	63.6	398	1	G3MSM	Ig gamma-3 chain C
23	794.5	63.1	444	2	PC4436	monoclonal antibod
24	789.5	62.7	324	1	G1MS	Ig gamma-1 chain C
25	784.5	62.3	326	2	PS0017	Ig gamma-1 chain C
26	784.5	62.3	393	1	G1MSM	Ig gamma-1 chain C
27	776.5	61.6	329	2	S00847	Ig gamma-2c chain
28	776	61.6	330	1	G2MSA	Ig gamma-2a chain
29	776	61.6	469	2	S37483	Ig gamma-2a chain
30	772	61.3	335	1	G2MSAB	Ig gamma-2a chain
31	771	61.2	399	1	G2MSAM	Ig gamma-2a chain
32	761	60.4	446	2	S40295	Ig gamma-2a chain
33	751.5	59.6	474	1	G2MS11	Ig gamma-2b chain
34	747.5	59.3	322	2	PS0019	Ig gamma-2a chain
35	746.5	59.2	405	1	G2MSBM	Ig gamma-2b chain
36	735	58.3	327	2	S06611	Ig gamma-2 chain C
37	731.5	58.1	475	2	S01321	Ig gamma-2b chain
38	669	53.1	180	2	I46732	Ig gamma heavy cha
39	549	43.6	249	2	S69340	Ig heavy chain VHI
40	547	43.4	218	2	A36040	Ig heavy chain V-I
41	542	43.0	152	2	S14236	Ig gamma-1 chain C
42	366.5	29.1	572	2	B46529	Ig Y heavy chain (
43	357	28.3	549	2	S04845	Ig heavy chain pre
44	353	28.0	343	2	S25644	Ig mu chain C regi
45	353	28.0	455	1	MHMS	Ig mu chain C regi

ALIGNMENTS

RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequenc
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,'
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

```
igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             97.2%;  Score 1225;  DB 1;  Length 330;
  Best Local Similarity   97.0%;  Pred. No. 3.5e-85;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| |||||||||||||||||||||:|:||||||||||||||||||||||
Db        159 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        279 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330


RESULT 2
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

  Query Match             96.7%;  Score 1219;  DB 2;  Length 374;
  Best Local Similarity   96.1%;  Pred. No. 1.2e-84;
  Matches  223;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
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Db        143 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 202

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| |||||||||||||||||||||:|:||||||||||||||||||||||
Db        203 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 262

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||:|:||||||||||||||||||||||||||||||||||||||
Db        263 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 322

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        323 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374


RESULT 3
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

  Query Match             96.6%;  Score 1217;  DB 4;  Length 255;
  Best Local Similarity   96.6%;  Pred. No. 1e-84;
  Matches  224;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 83

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| |||||||||||||||||||||:|:||||||||||||||||||||||
Db         84 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 143

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 203
```

```
y       181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
            ||||| |||||||||||||||||||||||||||||||||||||||| |:||||||||
>       204 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255


ESULT 4
T0207
g gamma chain C region - chimpanzee
;Species: Pan troglodytes (chimpanzee)
;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
;Accession: PT0207
;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
;l. Immunol. 28, 319-322, 1991
;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
;Reference number: PT0207; MUID:91287716; PMID:2062315
;Accession: PT0207
;Molecule type: mRNA
;Residues: 1-234 <EHR>
;Superfamily: immunoglobulin C region; immunoglobulin homology
;Keywords: immunoglobulin
;48-117/Domain: immunoglobulin homology <IMM>

 Query Match             93.0%;  Score 1172;  DB 2;  Length 234;
 Best Local Similarity   95.6%;  Pred. No. 2.3e-81;
 Matches  215;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

y         1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
            |||||| ||||||| |||||||||||||||||||||||||||||||||||||||||||||
>        10 EPKSCDTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 69

y         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
            |||||||||| |||||||||||||||||||||||:|:||||||||||||||||||||||
>        70 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 129

y        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
            ||||| ||||||||||||||||||||||||||||||||||||||:||||||||||
>       130 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTTP 189

y        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRS 225
            ||||| |||||||||||||||||||||||||||||||||||||| |:|
>       190 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 234


ESULT 5
23511
g gamma-3 chain C region (allotype G3m(b)) - human
Species: Homo sapiens (man)
Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
Accession: A23511
Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
ucleic Acids Res. 14, 1779-1789, 1986
Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cc
Reference number: A23511; MUID:86148507; PMID:3081877
Accession: A23511
Molecule type: DNA
Residues: 1-377 <HUC>
Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
Genetics:
Gene: GDB:IGHG3
Cross-references: GDB:119339; OMIM:147120
Map position: 14q32.33-14q32.33
Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
Superfamily: immunoglobulin C region; immunoglobulin homology
Keywords: immunoglobulin
20-85/Domain: immunoglobulin homology <IMM>

 Query Match             90.3%;  Score 1138;  DB 2;  Length 377;
 Best Local Similarity   89.7%;  Pred. No. 1.5e-78;
 Matches  208;  Conservative   11;  Mismatches   13;  Indels    0;  Gaps    0;

y         1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
            ||||||    || |||||||||||||||||||||||||||||||||||||||||||:|
>       146 EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 205

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||:|||||||||||:|:||||||||||||||||||||
Db        206 KWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 265

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||| | |||||||||||||:|:|||||||||||||||||||||||:||||||| |||
Db        266 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 325

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              |:||| |||||||||||||||||:||||||||||| : |:||||||||
Db        326 PMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPGK 377


RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 converte
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             90.2%;  Score 1136;  DB 2;  Length 377;
  Best Local Similarity   89.7%;  Pred. No. 2.1e-78;
  Matches  208;  Conservative   11;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||    || |||||||||||||||||||||||||||||||||||||||||||:|
Db        146 EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 205

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||:|||||||||||:|:||||||||||||||||||||
Db        206 KWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 265

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||| | |||||||||||||:|:|||||||||||||||||||||||:||||||| |||
Db        266 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 325

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||:|||||||||:|||||||||||| : |:||||||||
Db        326 PVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNRFTQKSLSLSPGK 377


RESULT 7
G3HUWI
Ig gamma-3 heavy chain disease proteins - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C;Accession: A90442; A92219; A90198; A93915; A02149
R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-c
A;Reference number: A90442; MUID:81021548; PMID:6774747
A;Contents: heavy chain disease protein Wis
A;Accession: A90442
A;Molecule type: protein
A;Residues: 1-289 <FRA>
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co
A;Note: the sequence of residues 42-76 was taken from the reference that follows
R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
```

```
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A;Reference number: A92219; MUID:77118561; PMID:402363
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
A;Accession: A92219
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
idue segment (12-28)
A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter
R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
A;Accession: A90198
A;Molecule type: protein
A;Residues: 59-125,'EB',128-226,228-289 <WOL>
A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A;Reference number: A93915; MUID:82247835; PMID:6808505
A;Contents: heavy chain disease protein Omm
A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein Wis is shown.
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             89.1%;  Score 1123;  DB 1;  Length 289;
  Best Local Similarity   88.3%;  Pred. No. 1.5e-77;
  Matches  204;  Conservative   14;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||    || |||||||||||||||||||||||||||||||||||||||||||:|
Db         59 EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 118

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              ||||||:||| |||||||:|:|||:|||||||||||||::|||||||||||||||||||
Db        119 KWYVDGVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKT 178

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||| | ||||||||||||||:|:|||||||||||||||||||||:||||||| |||
Db        179 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 238

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPG 231
              |:||| |||||||||||||||||:||||||||||| : |:|||||||
Db        239 PMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG 289


RESULT 8
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; I
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat:
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             87.9%;  Score 1107;  DB 1;  Length 326;
  Best Local Similarity   88.4%;  Pred. No. 2.8e-76;
  Matches  205;  Conservative   12;  Mismatches   11;  Indels    4;  Gaps    2;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              | | | :   |||||||  : |||||||||||||||||||||||||||||||||||:|
Db         99 ERKCCVE---CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 154

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| ||||||||:|||:|||||||:||:|:|||||||||||| ||||||||
Db        155 NWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKT 214

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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                ||| | ||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||
Db        215 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 274

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              |:||| |||||||||||||||||||||||||||||||| |:||||||||
Db        275 PMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326


RESULT 9
IHU
g gamma-4 chain C region - human
Species: Homo sapiens (man)
Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
Accession: A90933; A90249; A02150
Ellison, J.; Buxbaum, J.; Hood, L.
JA 1, 11-18, 1981
Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
Reference number: A90933; MUID:83157104; PMID:6299662
Accession: A90933
Molecule type: DNA
Residues: 1-327 <ELL>
Cross-references: UNIPROT:P01861
Note: the sequence was determined from the germline gene
Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
Reference number: A90249; MUID:70207560; PMID:4192699
Accession: A90249
Molecule type: protein
Residues: 1-30;81-326 <PIN>
Genetics:
Gene: GDB:IGHG4
Cross-references: GDB:119340; OMIM:147130
Map position: 14q32.33-14q32.33
Introns: 99/1; 111/1; 221/1
Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
ain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
Superfamily: immunoglobulin C region; immunoglobulin homology
Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
20-85/Domain: immunoglobulin homology <IM1>
99-110/Region: hinge
134-203/Domain: immunoglobulin homology <IM2>
240-307/Domain: immunoglobulin homology <IM3>
14/Disulfide bonds: interchain (to light chain) #status experimental
27-83,141-201,247-305/Disulfide bonds: #status predicted
106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
177/Binding site: carbohydrate (Asn) (covalent) #status predicted

 Query Match            87.1%;  Score 1097;  DB 1;  Length 327;
 Best Local Similarity   90.5%;  Pred. No. 1.6e-75;
 Matches  201;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
              || ||||| |||||||||||||||||||||||||||||||| ||||||:||||||||||
Db        106 CPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH 165

Qy         71 NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
              | ||||||||:|||||||||||||||:|:|||||||||||| ||: ||||||||| ||||
Db        166 NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE 225

Qy        131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSVGSFF 190
              |||||||||::|:|||||||||||||||||||||||||||||||||||||||||| ||||
Db        226 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 285

Qy        191 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              |||:|||||||||:|||||||||||||||||| |:||||| ||
Db        286 LYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327


RESULT 10
IRB
g gamma chain C region - rabbit
Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haploty
A;Reference number: A91749; MUID:84030930; PMID:6313520
A;Accession: A91749
A;Molecule type: mRNA
A;Residues: 1-323 <BER>
A;Cross-references: UNIPROT:P01870
A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R;Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobu
A;Reference number: A90290; MUID:76135469; PMID:1243651
A;Accession: A90290
A;Molecule type: protein
A;Residues: 1-47,'E',49-71,'PV',72-128 <PRA>
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A;Reference number: A93928; MUID:83299917; PMID:6193512
A;Accession: A93928
A;Molecule type: mRNA
A;Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>
A;Cross-references: GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112
A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marke
R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G
A;Reference number: A90245; MUID:70110015; PMID:5461106
A;Accession: A90245
A;Molecule type: protein
A;Residues: 132-143,'E',145-161 <FRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A;Reference number: A94416
A;Accession: A94416
A;Molecule type: protein
A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',2
A;Note: this has the e15 allotypic marker, 185-Ala
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-82/Domain: immunoglobulin homology <IM1>
F;130-199/Domain: immunoglobulin homology <IM2>
F;236-303/Domain: immunoglobulin homology <IM3>
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            70.1%;  Score 883;  DB 1;  Length 323;
  Best Local Similarity   64.5%;  Pred. No. 2.2e-59;
  Matches  160;  Conservative   34;  Mismatches   38;  Indels   16;  Gaps    2;

Qy          1 EPKSCDKTH--------------TC--PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV 44
              :| :|:  |                ||  | || ||||||||||:||||||||||||||||
Db         76 QPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVFIFPPKPKDTLMISRTPEV 135

Qy         45 TCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEY 104
              |||||||| :||||:| ||::  :|   :   ||:|:||| |||| | : ||:|: |||:
Db        136 TCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLPITHQDWLRGKEF 195

Qy        105 KCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 164
              |||| |||||||||||||: || ||:|||: | |:||:   |||||:: |||||||:|
Db        196 KCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISV 255

Qy        165 EWESNGQPENNYKTTPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQR 224
              ||| ||: |:|||||| |||| ||:|||:||:|  | ||:|:||:|||||||||||| |:
Db        256 EWEKNGKAEDNYKTTPAVLDSDGSYFLYNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQK 315

Qy        225 SLSLSPGK 232
              |:| ||||
Db        316 SISRSPGK 323
```

RESULT 11
I47160
Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 2.8e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;

Qy 11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
Db 106 CPICPACE-SPGPSVFIFPPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH 164

Qy 71 NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
Db 165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE 224

Qy 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS 188
Db 225 PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT 284

Qy 189 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
Db 285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328

RESULT 12
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 2.8e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;

Qy 11 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
Db 106 CPICPACE-SPGPSVFIFPPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVH 164

Qy 71 NVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
Db 165 TAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTRE 224

Qy 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVGS 188
Db 225 PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGT 284

Qy 189 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
Db 285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328

RESULT 13
I47162
Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47162
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C;Genetics:
A;Gene: IgG4
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 865; DB 2; Length 277;
Best Local Similarity 69.0%; Pred. No. 4.1e-58;
Matches 158; Conservative 32; Mismatches 35; Indels 4; Gaps 3;

Qy 8 THTCPPCP-APELLG-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65
Db 49 TKTKPPCPICPACEGPGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYVD 108

Qy 66 GVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAK 125
Db 109 GVEVHTAQTRPKEEQFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAK 168

Qy 126 VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVL 183
Db 169 GQTREPQVYTLPPPTEELSRSKVTLTCLVTGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQ 228

Qy 184 DSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
Db 229 DVDGTYFLYSKLAVDKASWQRGDTFQCAVMHEALHNHYTQKSIFKTPGK 277

RESULT 14
G2GP
Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151
R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
A;Accession: A94553
A;Molecule type: protein
A;Residues: 1-3 <TRI>
A;Cross-references: UNIPROT:P01862
R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Ar
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
A;Molecule type: protein
A;Residues: 4-68 <BIR>
R;Turner, K.J.; Cebra, J.J.

.ochemistry 10, 9-17, 1971
Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ami
Reference number: A90359; MUID:71058486; PMID:5538616
Accession: A90359
Molecule type: protein
Residues: 69-133;312-329 <TUR>
Tracey, D.E.; Cebra, J.J.
.ochemistry 13, 4796-4803, 1974
Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
Reference number: A90384; MUID:75036072; PMID:4429665
Accession: A90384
Molecule type: protein
Residues: 134-226 <TRA>
Trischmann, T.M.; Cebra, J.J.
.ochemistry 13, 4804-4811, 1974
Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
Reference number: A90385; MUID:75036073; PMID:4609467
Accession: A90385
Molecule type: protein
Residues: 227-311 <TR2>
Oliveira, B.; Lamm, M.E.
.ochemistry 10, 26-31, 1971
Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
Reference number: A90354; MUID:71058474; PMID:4922544
Contents: annotation; disulfide bonds
Note: Cys-16 is involved in a heavy-light chain bond
Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
in disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
Superfamily: immunoglobulin C region; immunoglobulin homology
Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
21-81/Domain: immunoglobulin homology <IM1>
135-204/Domain: immunoglobulin homology <IM2>
241-310/Domain: immunoglobulin homology <IM3>
28-79/Disulfide bonds: #status experimental
142-202/Disulfide bonds: #status experimental
178/Binding site: carbohydrate (Asn) (covalent) #status experimental
248-308/Disulfide bonds: #status experimental

Query Match 68.1%; Score 858; DB 1; Length 329;
Best Local Similarity 67.4%; Pred. No. 1.7e-57;
Matches 157; Conservative 28; Mismatches 42; Indels 6; Gaps 2;

```
Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              :|  |    ||| || || |||||||:||||||||||||| || |||||||| ::|||:|
Db        101 ZPBPC----TCPKCPPPENLGGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQF 156

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
               |:||   | | :|||| ||||:|:|| ||| : ||:|: |||:|||| ||||||||||
Db        157 TWFVDNKPVGNAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKT 216

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKT 178
              ||| |  || | ||||||||||:|::||:|||:  |:|:|| ||| ||  |  |  ||
Db        217 ISKTKGAPRMPDVYTLPPSRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKN 276

Qy        179 TPPVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPG 231
              |||: |: ||:||||||||||| | || |::||||||||||||  |:::| |||
Db        277 TPPIEDADGSYFLYSKLTVDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
```

ESULT 15
47158
g gamma 1 chain constant region - pig (fragment)
;Species: Sus scrofa domestica (domestic pig)
;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
;Accession: I47158
;Kacskovics, I.; Sun, J.; Butler, J.E.
. Immunol. 153, 3565-3573, 1994
;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
;Reference number: I47158; MUID:95015845; PMID:7930579
;Accession: I47158
;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122
C;Genetics:
A;Gene: IgG1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 847.5; DB 2; Length 328;
Best Local Similarity 69.3%; Pred. No. 1.1e-56;
Matches 156; Conservative 30; Mismatches 36; Indels 3; Gaps 2;

```
Qy         10 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 69
              ||| ||  | : |||||:||||||||||||:|||||||||||| |  ||:|:|||||||
Db        105 TCPICPGCE-VAGPSVFIFPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQFSWYVDGVEV 163

Qy         70 HNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPR 129
              |  :|:|:|||:|||||||||| : ||:|: |||:||||:|  ||||| :|||||  | |
Db        164 HTAETRPKEEQFNSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSR 223

Qy        130 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSVG 187
              |||||||||  :||::::|:|||||| |||| || |||:||||  ||| |:|||  |  |
Db        224 EPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVDG 283

Qy        188 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              :|||||| |||:||  |: | |:|||||||||| |:|:| : ||
Db        284 TFFLYSKLAVDKARWDHGDKFECAVMHEALHNHYTQKSISKTQGK 328
```

Search completed: October 27, 2004, 17:04:51
Job time : 21.7278 secs

GenCore version 5.1.6

protein - protein search, using sw model

on: October 27, 2004, 16:32:53 ; Search time 105.267 Seconds
(without alignments)
1268.081 Million cell updates/sec

tle: US-10-000-439-3
rfect score: 1260
quence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNHYQQRSLSLSPGK 232

oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 1825181 seqs, 575374646 residues

tal number of hits satisfying chosen parameters: 1825181

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

tabase : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1225	97.2	330	1	GC1_HUMAN	P01857 homo sapien
2	1225	97.2	407	2	BAC85237	Bac85237 homo sapi
3	1225	97.2	447	2	BAC86226	Bac86226 homo sapi
4	1225	97.2	464	2	AAH19337	Aah19337 homo sapi
5	1225	97.2	465	2	Q6GMX6	Q6gmx6 homo sapien
6	1225	97.2	466	2	Q6IN78	Q6in78 homo sapien
7	1225	97.2	466	2	AAH64496	Aah64496 homo sapi
8	1225	97.2	467	2	BAC85173	Bac85173 homo sapi
9	1225	97.2	467	2	AAH37361	Aah37361 homo sapi
10	1225	97.2	468	2	BAC85175	Bac85175 homo sapi
11	1225	97.2	468	2	BAC85444	Bac85444 homo sapi
12	1225	97.2	469	2	Q7Z7P5	Q7z7p5 homo sapien
13	1225	97.2	470	2	Q6PJA4	Q6pja4 homo sapien
14	1225	97.2	470	2	Q7Z5W1	Q7z5w1 homo sapien
15	1225	97.2	470	2	BAC85235	Bac85235 homo sapi
16	1225	97.2	470	2	BAC85387	Bac85387 homo sapi
17	1225	97.2	470	2	AAH62336	Aah62336 homo sapi
18	1225	97.2	470	2	AAH14258	Aah14258 homo sapi
19	1225	97.2	470	2	AAH18747	Aah18747 homo sapi
20	1225	97.2	470	2	AAH25314	Aah25314 homo sapi
21	1225	97.2	471	2	BAC85388	Bac85388 homo sapi
22	1225	97.2	471	2	AAH24289	Aah24289 homo sapi
23	1225	97.2	471	2	BAC05014	Bac05014 homo sapi
24	1225	97.2	472	2	Q6N089	Q6n089 homo sapien
25	1225	97.2	472	2	CAE45781	Cae45781 homo sapi
26	1225	97.2	472	2	BAC85232	Bac85232 homo sapi
27	1225	97.2	472	2	BAC86225	Bac86225 homo sapi
28	1225	97.2	473	2	BAC05013	Bac05013 homo sapi
29	1225	97.2	474	2	BAC85171	Bac85171 homo sapi
30	1225	97.2	474	2	BAC85401	Bac85401 homo sapi
31	1225	97.2	474	2	BAC05012	Bac05012 homo sapi
32	1225	97.2	475	2	Q6GMW7	Q6gmw7 homo sapien
33	1225	97.2	475	2	AAH26038	Aah26038 homo sapi
34	1225	97.2	476	2	Q6GMX1	Q6gmx1 homo sapien
35	1225	97.2	476	2	BAC05017	Bac05017 homo sapi
36	1225	97.2	477	2	BAC85394	Bac85394 homo sapi
37	1225	97.2	477	2	BAC85697	Bac85697 homo sapi
38	1225	97.2	477	2	BAC05018	Bac05018 homo sapi
39	1225	97.2	478	2	BAC85174	Bac85174 homo sapi
40	1225	97.2	478	2	BAC85436	Bac85436 homo sapi
41	1225	97.2	478	2	BAC86514	Bac86514 homo sapi
42	1225	97.2	479	2	AAH06402	Aah06402 homo sapi
43	1225	97.2	479	2	AAH14667	Aah14667 homo sapi
44	1225	97.2	679	2	Q96PQ8	Q96pq8 homo sapien
45	1224	97.1	474	2	BAC85350	Bac85350 homo sapi

ALIGNMENTS

RESULT 1
GC1_HUMAN
ID GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;

```
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT   characterization of the protein, the L- and H-chains, the cyanogen
RT   bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=81208100; PubMed=7236608;
RA   Deisenhofer J.;
RT   "Crystallographic refinement and atomic models of a human Fc fragment
RT   and its complex with fragment B of protein A from Staphylococcus
RT   aureus at 2.9- and 2.8-A resolution.";
RL   Biochemistry 20:2361-2370(1981).
CC   -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC       G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC       G1M(3) marker and the G1M (non-1) markers.
CC   -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC       116, 198, 269 and 272.
CC   -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC       155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC       268-272.
CC   -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC       residues 198, 267 and 272.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00228; AAC82527.1; ALT_INIT.
DR   PIR; A93433; GHHU.
DR   PDB; 1AJ7; X-ray; H=1-103.
DR   PDB; 1D5B; X-ray; B/H=1-101.
DR   PDB; 1D5I; X-ray; H=1-101.
DR   PDB; 1D6V; X-ray; H=1-101.
DR   PDB; 1DN2; X-ray; A/B=120-326.
DR   PDB; 1E4K; X-ray; A/B=106-329.
DR   PDB; 1FC1; X-ray; A/B=106-329.
DR   PDB; 1FC2; X-ray; D=106-329.
DR   PDB; 1FCC; X-ray; A=121-326.
DR   PDB; 1HZH; X-ray; H/K=1-330.
DR   PDB; 1I7Z; X-ray; B/D=1-103.
DR   PDB; 1IIS; X-ray; A/B=107-330.
DR   PDB; 1IIX; X-ray; A/B=107-330.
DR   PDB; 1L6X; X-ray; A=120-326.
DR   PDB; 1OQX; X-ray; A/B=119-330.
DR   PDB; 2RCS; X-ray; H=1-103.
DR   Genew; HGNC:5525; IGHG1.
DR   MIM; 147100; -.
DR   GO; GO:0005624; C:membrane fraction; NAS.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 2.
KW   3D-structure; Direct protein sequencing; Glycoprotein;
KW   Immunoglobulin C region; Immunoglobulin domain.
FT   NON_TER       1      1
FT   DOMAIN        1     98       CH1.
FT   DOMAIN       99    110       Hinge.
FT   DOMAIN      111    223       CH2.
FT   DOMAIN      224    330       CH3.
FT   DISULFID     27     83
FT   DISULFID    103    103       Interchain (with light chain).
FT   DISULFID    109    109       Interchain (with heavy chain).
FT   DISULFID    112    112       Interchain (with heavy chain).
FT   DISULFID    144    204
FT   DISULFID    250    308
FT   CARBOHYD    180    180       N-linked (GlcNAc. . .).
FT   VARIANT      97     97       K -> R (in G1M(3) marker).
FT                                /FTId=VAR_003886.
FT   VARIANT     239    239       D -> E (in G1M(non-1) marker).
FT                                /FTId=VAR_003887.
FT   VARIANT     241    241       L -> M (in G1M(non-1) marker).
FT                                /FTId=VAR_003888.
FT   STRAND       23     24
FT   STRAND       26     33
FT   STRAND       38     38
FT   STRAND       41     41
FT   TURN         42     45
FT   TURN         48     49
FT   STRAND       50     52
FT   STRAND       57     58
FT   TURN         59     61
FT   STRAND       62     71
FT   HELIX        73     75
FT   TURN         76     78
FT   STRAND       82     87
FT   TURN         88     91
FT   STRAND       92     97
FT   TURN        102    103
FT   STRAND      122    126
FT   HELIX       130    134
FT   TURN        136    137
FT   STRAND      141    149
FT   STRAND      157    162
FT   TURN        163    164
FT   STRAND      165    167
FT   STRAND      171    172
FT   STRAND      176    177
FT   TURN        179    180
FT   STRAND      183    190
FT   HELIX       193    197
FT   TURN        198    199
FT   STRAND      202    207
FT   TURN        209    210
FT   STRAND      215    219
FT   STRAND      227    227
FT   STRAND      230    234
FT   HELIX       238    242
FT   STRAND      245    256
FT   STRAND      261    266
FT   TURN        267    268
FT   STRAND      269    270
FT   STRAND      274    276
FT   STRAND      280    281
FT   TURN        283    284
FT   STRAND      287    296
FT   HELIX       297    301
FT   TURN        302    303
FT   STRAND      306    311
FT   TURN        313    314
FT   HELIX       316    318
FT   STRAND      319    324
SQ   SEQUENCE   330 AA;  36106 MW;  3770EE106C2FA33D CRC64;

  Query Match             97.2%;  Score 1225;  DB 1;  Length 330;
  Best Local Similarity   97.0%;  Pred. No. 1.8e-89;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
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Qy          61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
               |||||||||||  |||||||||||||||||||||||:|:||||||||||||||||||||||
Db         159 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218

Qy         121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
               |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278

Qy         181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
               |||||  |||||||||||||||||||||||||||||||||||||||||:|||||||||
Db         279 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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ESULT 2
AC85237
ID BAC85237 PRELIMINARY; PRT; 407 AA.
AC BAC85237;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA FLJ26298 fis, clone DMC07404, highly similar to Ig gamma-1 chain
DE C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dermoid tumor;
RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK129809; BAC85237.1; -.
SQ SEQUENCE 407 AA; 44159 MW; DB8E4D367B456FCE CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 407;
Best Local Similarity 97.0%; Pred. No. 2.3e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy           1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         176 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 235

Qy          61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
               |||||||||||  |||||||||||||||||||||||:|:||||||||||||||||||||||
Db         236 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 295

Qy         121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
               |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         296 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 355

Qy         181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
               |||||  |||||||||||||||||||||||||||||||||||||||||:|||||||||
Db         356 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 407
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ESULT 3
AC86226
ID BAC86226 PRELIMINARY; PRT; 447 AA.
AC BAC86226;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA FLJ43645 fis, clone SYNOV3000302, highly similar to Ig gamma-1
DE chain C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Synovial membrane tissue;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK125633; BAC86226.1; -.
SQ SEQUENCE 447 AA; 49289 MW; F28884C17E89E8EF CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 447;
Best Local Similarity 97.0%; Pred. No. 2.5e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy           1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         216 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 275

Qy          61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
               |||||||||||  |||||||||||||||||||||||:|:||||||||||||||||||||||
Db         276 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 335

Qy         121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
               |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         336 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 395

Qy         181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
               |||||  |||||||||||||||||||||||||||||||||||||||||:|||||||||
Db         396 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447
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RESULT 4
AAH19337
ID AAH19337 PRELIMINARY; PRT; 464 AA.
AC AAH19337;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019337; AAH19337.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   464 AA;  50891 MW;  2F80673E74E2A485 CRC64;

  Query Match             97.2%;  Score 1225;  DB 2;  Length 464;
  Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 292

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| |||||||||||||||||||:|:||||||||||||||||||||||||
Db        293 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 352

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 412

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        413 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 464


RESULT 5
Q6GMX6
ID   Q6GMX6      PRELIMINARY;      PRT;   465 AA.
AC   Q6GMX6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073766; AAH73766.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51083 MW;  B3A9B7D0FDB1386E CRC64;

  Query Match             97.2%;  Score 1225;  DB 2;  Length 465;
  Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 293

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| |||||||||||||||||||:|:||||||||||||||||||||||||
Db        294 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 353

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 413

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        414 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 465


RESULT 6
Q6IN78
ID   Q6IN78      PRELIMINARY;      PRT;   466 AA.
AC   Q6IN78;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHG1 protein.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
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?   SEQUENCE FROM N.A.
?   TISSUE=Peripheral Nervous System;
\   Strausberg R.;
    Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
?   EMBL; BC072419; AAH72419.1; -.
?   InterPro; IPR003599; Ig.
?   InterPro; IPR007110; Ig-like.
?   InterPro; IPR003597; Ig_c1.
?   InterPro; IPR003006; Ig_MHC.
?   InterPro; IPR003596; Ig_v.
?   Pfam; PF07654; C1-set; 3.
?   Pfam; PF00047; ig; 4.
?   SMART; SM00409; IG; 2.
?   SMART; SM00407; IGc1; 3.
?   SMART; SM00406; IGv; 1.
?   PROSITE; PS50835; IG_LIKE; 4.
?   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
)   SEQUENCE   466 AA;  50853 MW;  53EB0BCEDE81076E CRC64;

 Query Match             97.2%;  Score 1225;  DB 2;  Length 466;
 Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
 Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

/          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
>        235 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 294

/         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
             |||||||||||  |||||||||||||||||||||||:|:|||||||||||||||||||||
>        295 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 354

/        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
             |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
>        355 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 414

/        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
             |||||  |||||||||||||||||||||||||||||||||  |:||||||||
>        415 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466


ESULT 7
AH64496
)   AAH64496     PRELIMINARY;      PRT;   466 AA.
:   AAH64496;
I   02-MAR-2004 (TrEMBLrel. 27, Created)
I   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
I   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
E   Hypothetical protein.
S   Homo sapiens (Human).
C   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X   NCBI_TaxID=9606;
N   [1]
P   SEQUENCE FROM N.A.
C   TISSUE=Spleen;
K   MEDLINE=22388257; PubMed=12477932;
A   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A   Jones S.J., Marra M.A.;
R   "Generation and initial analysis of more than 15,000 full-length human
R   and mouse cDNA sequences.";
L   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
N   [2]
P   SEQUENCE FROM N.A.
C   TISSUE=Spleen;
A   Strausberg R.;
L   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
R   EMBL; BC064496; AAH64496.1; -.
W   Hypothetical protein.
Q   SEQUENCE   466 AA;  51078 MW;  13F032EDAC9DBC22 CRC64;

  Query Match             97.2%;  Score 1225;  DB 2;  Length 466;
  Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 294

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||  |||||||||||||||||||||||:|:|||||||||||||||||||||
Db        295 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 354

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 414

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              |||||  |||||||||||||||||||||||||||||||||  |:||||||||
Db        415 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466


RESULT 8
BAC85173
ID   BAC85173     PRELIMINARY;      PRT;   467 AA.
AC   BAC85173;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CDNA FLJ26001 fis, clone DMC07585, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dermoid tumor;
RA   Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA   Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK129512; BAC85173.1; -.
SQ   SEQUENCE   467 AA;  50782 MW;  632AEA2D6CD248F5 CRC64;

  Query Match             97.2%;  Score 1225;  DB 2;  Length 467;
  Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 295

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||  |||||||||||||||||||||||:|:|||||||||||||||||||||
Db        296 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 355

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 415
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Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||||||||| |:||||||||
Db        416 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 9
AAH37361
ID   AAH37361    PRELIMINARY;      PRT;   467 AA.
AC   AAH37361;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC037361; AAH37361.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   467 AA;  51129 MW;  20F0F71415B25E48 CRC64;

  Query Match             97.2%;  Score 1225;  DB 2;  Length 467;
  Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 295

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||||:|:|||||||||||||||||||||||
Db        296 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 355

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 415

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| ||||||||||||||||||||||||||||||||||||||| |:||||||||
Db        416 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467


RESULT 10
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BAC85175
ID   BAC85175    PRELIMINARY;      PRT;   468 AA.
AC   BAC85175;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CDNA FLJ26006 fis, clone DMC08725, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dermoid tumor;
RA   Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA   Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK129517; BAC85175.1; -.
SQ   SEQUENCE   468 AA;  51266 MW;  11C519D86AE3D44B CRC64;

  Query Match             97.2%;  Score 1225;  DB 2;  Length 468;
  Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 296

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||||:|:|||||||||||||||||||||||
Db        297 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 356

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 416

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| ||||||||||||||||||||||||||||||||||||||| |:||||||||
Db        417 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 468


RESULT 11
BAC85444
ID   BAC85444    PRELIMINARY;      PRT;   468 AA.
AC   BAC85444;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CDNA FLJ27334 fis, clone TMS09201, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymus;
RA   Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
RA   Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA   Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
RA   Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK130844; BAC85444.1; -.
SQ   SEQUENCE   468 AA;  51224 MW;  9280ACAD6817FC20 CRC64;

  Query Match             97.2%;  Score 1225;  DB 2;  Length 468;
  Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;
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Y          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
D        237 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 296

Y         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
           |||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||||||
D        297 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 356

Y        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
D        357 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 416

Y        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
           ||||| |||||||||||||||||||||||||||||| :||||||||
D        417 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 468
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ESULT 12
7Z7P5
D   Q7Z7P5      PRELIMINARY;      PRT;   469 AA.
C   Q7Z7P5;
T   01-OCT-2003 (TrEMBLrel. 25, Created)
T   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
T   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
E   IGHG1 protein.
G   Homo sapiens (Human).
C   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X   NCBI_TaxID=9606;
N   [1]
P   SEQUENCE FROM N.A.
C   TISSUE=Spleen;
X   MEDLINE=22388257; PubMed=12477932;
A   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A   Jones S.J., Marra M.A.;
T   "Generation and initial analysis of more than 15,000 full-length human
T   and mouse cDNA sequences.";
L   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
N   [2]
P   SEQUENCE FROM N.A.
C   TISSUE=Spleen;
A   Strausberg R.;
L   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
R   EMBL; BC051328; AAH51328.1; -.
R   InterPro; IPR007110; Ig-like.
R   InterPro; IPR003597; Ig_c1.
R   InterPro; IPR003006; Ig_MHC.
R   InterPro; IPR003596; Ig_v.
R   Pfam; PF07654; C1-set; 3.
R   Pfam; PF00047; ig; 1.
R   SMART; SM00406; IGv; 1.
R   PROSITE; PS50835; IG_LIKE; 4.
R   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Q   SEQUENCE   469 AA;  51395 MW;  C8D5BE12BAAF795C CRC64;

 Query Match             97.2%;  Score 1225;  DB 2;  Length 469;
 Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
```

```
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 297

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||||||
Db        298 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 357

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 417

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||| :||||||||
Db        418 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 469
```

```
RESULT 13
Q6PJA4
ID   Q6PJA4      PRELIMINARY;      PRT;   470 AA.
AC   Q6PJA4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018747; AAH18747.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
```

```
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51715 MW;  7B49556A11FD7D99 CRC64;

  Query Match             97.2%;  Score 1225;  DB 2;  Length 470;
  Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||||:|:||||||||||||||||||||
Db        299 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 418

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 14
Q7Z5W1
ID   Q7Z5W1      PRELIMINARY;      PRT;   470 AA.
AC   Q7Z5W1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053984; AAH53984.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51204 MW;  778CF34521483E1A CRC64;

  Query Match             97.2%;  Score 1225;  DB 2;  Length 470;
  Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||||:|:||||||||||||||||||||
Db        299 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 418

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 15
BAC85235
ID   BAC85235    PRELIMINARY;      PRT;   470 AA.
AC   BAC85235;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CDNA FLJ26276 fis, clone DMC06522, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dermoid tumor;
RA   Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA   Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK129787; BAC85235.1; -.
SQ   SEQUENCE   470 AA;  51090 MW;  460F4717D4528A16 CRC64;

  Query Match             97.2%;  Score 1225;  DB 2;  Length 470;
  Best Local Similarity   97.0%;  Pred. No. 2.7e-89;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||||:|:||||||||||||||||||||
Db        299 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 418

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


Search completed: October 27, 2004, 17:03:56
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ob time : 106.267 secs

GenCore version 5.1.6

protein - protein search, using sw model

un on: October 27, 2004, 16:31:18 ; Search time 88.7544 Seconds
(without alignments)
937.702 Million cell updates/sec

itle: US-10-000-439-3
erfect score: 1260
equence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNHYQQRSLSLSPGK 232

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

earched: 2002273 seqs, 358729299 residues

otal number of hits satisfying chosen parameters: 2002273

inimum DB seq length: 0
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description
1	1260	100.0	232	6	AAO19665	Aao19665 Human IgG
2	1260	100.0	330	6	AAO19664	Aao19664 Human IgG
3	1260	100.0	569	6	AAO19668	Aao19668 GE2 fusio
4	1225	97.2	232	2	AAW26232	Aaw26232 Human IgG
5	1225	97.2	232	3	AAB28690	Aab28690 Human IgG
6	1225	97.2	232	4	AAB80897	Aab80897 Human IgG
7	1225	97.2	232	4	AAY72915	Aay72915 Human par
8	1225	97.2	232	5	AAE15347	Aae15347 Human imm
9	1225	97.2	232	5	AAE26272	Aae26272 Human IgG
10	1225	97.2	232	7	ADJ65991	Adj65991 Herpes vi
11	1225	97.2	232	8	ADJ57512	Adj57512 Human IgG
12	1225	97.2	233	5	ABB09463	Abb09463 Human IgG
13	1225	97.2	235	6	ABJ38647	Abj38647 pCXFc pro
14	1225	97.2	235	6	ADA89055	Ada89055 Plasmid p
15	1225	97.2	235	7	ADD25647	Add25647 Binding d
16	1225	97.2	235	7	ADG74307	Adg74307 Fibroblas
17	1225	97.2	247	5	AAE26274	Aae26274 Human bet
18	1225	97.2	251	5	ABB81490	Abb81490 Human imm
19	1225	97.2	251	6	AAE35214	Aae35214 Human wil
20	1225	97.2	259	2	AAY24154	Aay24154 Protein f
21	1225	97.2	267	5	AAE26273	Aae26273 Human tPA
22	1225	97.2	269	8	ADJ52120	Adj52120 CH1 delet
23	1225	97.2	287	4	AAB47590	Aab47590 Fusion pr
24	1225	97.2	329	2	AAR91806	Aar91806 Human imm
25	1225	97.2	330	4	AAB04071	Aab04071 Zcytor 10
26	1225	97.2	330	5	AAM47856	Aam47856 Human Ig-
27	1225	97.2	330	5	AAE21960	Aae21960 Human dea
28	1225	97.2	330	5	ABB81641	Abb81641 Human IgG
29	1225	97.2	330	5	ABB05736	Abb05736 Human imm
30	1225	97.2	330	6	ABP71856	Abp71856 Human IgG
31	1225	97.2	330	6	AAE32915	Aae32915 Human imm
32	1225	97.2	330	6	AAE32627	Aae32627 Human imm
33	1225	97.2	330	6	ABR82103	Abr82103 Human DR6
34	1225	97.2	330	6	AAO31102	Aao31102 Human A2-
35	1225	97.2	330	6	ABR55836	Abr55836 Anti-Ang-
36	1225	97.2	330	6	AAO30893	Aao30893 Human imm
37	1225	97.2	330	7	ADF11389	Adf11389 Anti-OPGL
38	1225	97.2	330	7	ADE97351	Ade97351 Human IgG
39	1225	97.2	330	7	ADF83605	Adf83605 Cytokine
40	1225	97.2	330	7	ADF75001	Adf75001 Human Ig
41	1225	97.2	330	8	ADM41537	Adm41537 Anti-inte
42	1225	97.2	330	8	ADM68911	Adm68911 Human IgG
43	1225	97.2	330	8	ADN36570	Adn36570 Chemokine
44	1225	97.2	330	8	ADN97485	Adn97485 Artificia
45	1225	97.2	331	3	AAY91106	Aay91106 Human TR-

ALIGNMENTS

RESULT 1
AAO19665
ID AAO19665 standard; protein; 232 AA.
XX
AC AAO19665;
XX
DT 28-MAR-2003 (first entry)
XX
DE Human IgG1 heavy chain constant region hinge-CH2-CH3 portion.
XX
KW Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
KW Fcepsilon receptor; autoimmune disease; constant region; heavy chain;
KW antiasthmatic; antiallergic; antiinflammatory; dermatological;
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;
KW hinge-CH2-CH3 region.
XX
OS Homo sapiens.
XX
PN WO200288317-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-US013527.
XX
PR 01-MAY-2001; 2001US-00847208.
PR 24-OCT-2001; 2001US-00000439.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Saxon A, Zhang K, Zhu D;
XX
DR WPI; 2003-103456/09.
XX
PT New fusion molecules comprising polypeptide sequences that bind to IgG
PT inhibitory receptor and native IgE receptor, useful for treating IgE-
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
PT autoimmune diseases.
XX
PS Claim 19; Fig 3; 116pp; English.
XX
CC The present invention relates to a fusion molecule comprising a first
CC polypeptide sequence capable of specific binding to a native IgG
CC inhibitory receptor consisting of an immune receptor tyrosine-based
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
CC functionally connected to a second polypeptide sequence capable of
CC specific binding directly or indirectly to a native IgE receptor
CC (FcepsilonR). Also provided are nucleotide sequences encoding such a
CC fusion protein. The fusion molecules and compositions are useful for

CC treating an IgE-mediated biological response, preferably an IgE-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is the human IgG1
CC heavy chain constant region hinge-CH2-CH3 portion
XX
SQ Sequence 232 AA;

Query Match 100.0%; Score 1260; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.8e-91;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy 61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232

RESULT 2
AAO19664
ID AAO19664 standard; protein; 330 AA.
XX
AC AAO19664;
XX
DT 28-MAR-2003 (first entry)
XX
DE Human IgG1 heavy chain constant region.
XX
KW Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
KW Fcepsilon receptor; autoimmune disease; constant region; heavy chain;
KW antiasthmatic; antiallergic; antiinflammatory; dermatological;
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200288317-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-US013527.
XX
PR 01-MAY-2001; 2001US-00847208.
PR 24-OCT-2001; 2001US-00000439.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Saxon A, Zhang K, Zhu D;
XX
DR WPI; 2003-103456/09.
XX
PT New fusion molecules comprising polypeptide sequences that bind to IgG
PT inhibitory receptor and native IgE receptor, useful for treating IgE-
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
PT autoimmune diseases.
XX
PS Claim 64; Fig 2; 116pp; English.
XX
CC The present invention relates to a fusion molecule comprising a first
CC polypeptide sequence capable of specific binding to a native IgG
CC inhibitory receptor consisting of an immune receptor tyrosine-based
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
CC functionally connected to a second polypeptide sequence capable of
CC specific binding directly or indirectly to a native IgE receptor
CC (FcepsilonR). Also provided are nucleotide sequences encoding such a
CC fusion protein. The fusion molecules and compositions are useful for
CC treating an IgE-mediated biological response, preferably an IgE-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is the human IgG1
CC heavy chain constant region
XX
SQ Sequence 330 AA;

Query Match 100.0%; Score 1260; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 4.2e-91;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158

Qy 61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
Db 159 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 218

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 219 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
Db 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 330

RESULT 3
AAO19668
ID AAO19668 standard; protein; 569 AA.
XX
AC AAO19668;
XX
DT 28-MAR-2003 (first entry)
XX
DE GE2 fusion protein for use in treating immune diseases.
XX
KW Human; IgE; immunoglobulin E; immunotherapy; immune disease;
KW Fcepsilon receptor; autoimmune disease; constant region; heavy chain;
KW antiasthmatic; antiallergic; antiinflammatory; dermatological; GE2;
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;
KW fusion protein.
XX
OS Synthetic.
OS Unidentified.
XX
PN WO200288317-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-US013527.
XX
PR 01-MAY-2001; 2001US-00847208.
PR 24-OCT-2001; 2001US-00000439.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Saxon A, Zhang K, Zhu D;
XX
DR WPI; 2003-103456/09.
XX
PT New fusion molecules comprising polypeptide sequences that bind to IgG

inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

Claim 35; Fig 7; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FcepsilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is a gammahinge-CHgamma2-CHgamma3-(Gly4Ser)3-CHepsilon2-CHepsilon3-CHepsilon3 fusion protein (designated GE2) of the invention

Sequence 569 AA;

```
Query Match             100.0%;  Score 1260;  DB 6;  Length 569;
Best Local Similarity   100.0%;  Pred. No. 8.1e-91;
Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120

        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
```

RESULT 4
AAW26232
AAW26232 standard; protein; 232 AA.

AAW26232;

16-MAR-1998 (first entry)

Human IgG1 hinge/Fc region.

Fusion protein; hydrophilic spacer; recombinant; expression system; carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.

Homo sapiens.

WO9728272-A1.

07-AUG-1997.

31-JAN-1997; 97WO-US001470.

31-JAN-1996; 96US-00595043.

(TECH-) TECHNOLOGENE INC.

Sgarlato GD;

XX
DR WPI; 1997-402624/37.
DR N-PSDB; AAT80158.
XX
PT Recombinant protein expression system for fusion protein production -
PT useful for high quantity production of authentic recombinant proteins.
XX
PS Example 3; Page 133-134; 194pp; English.
XX
CC A novel recombinant vector has been developed which comprises a
CC nucleotide sequence encoding a fusion protein. The fusion protein
CC comprises three domains joined together in order, from N-terminus to C-
CC terminus, of a first domain comprising a protein of interest, a second
CC domain comprising a hydrophilic spacer and an affinity domain, each
CC domain comprising amino acid residues. The present sequence represents
CC the hinge/Fc region of human IgG1, used in example 3 of the present
CC invention. The recombinant vector is used for the production of authentic
CC recombinant proteins of interest. The method of the invention is useful
CC for the expression of fusion proteins capable of isolation by affinity
CC chromatography in pro- or eukaryotic cells. This method allows for the
CC efficient cleavage and generation of authentic proteins of interest that
CC do not contain extraneous (i.e. non-naturally occurring) amino acids
XX
SQ Sequence 232 AA;

```
  Query Match             97.2%;  Score 1225;  DB 2;  Length 232;
  Best Local Similarity   97.0%;  Pred. No. 1.6e-88;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||:|:||||||||||||||||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
```

RESULT 5
AAB28690
ID AAB28690 standard; protein; 232 AA.
XX
AC AAB28690;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human IgGgamma1 hinge, CH2 and CH3 regions.
XX
KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
KW transplant rejection; cardiovascular disease; arteriosclerosis;
KW IgGgamma1.
XX
OS Homo sapiens.
XX
PN WO200063253-A1.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008004.
XX
PR 16-APR-1999; 99US-00293245.
XX

PA (AMGE-) AMGEN INC.
XX
PI Hsu H, Meng S;
XX
DR WPI; 2000-665240/64.
XX
PT Fusion protein of AGP-1 protein and an Fc region, used to treat
PT proliferative disorders, immune disorders, and virally-induced disorders.
XX
PS Claim 2; Fig 1; 93pp; English.
XX
CC The present sequence was used in the production of AGP-1 fusion proteins.
CC AGP-1 is a type II transmembrane protein. The fusion proteins comprise an
CC Fc immunoglobulin region fused to the N-terminal portion of the AGP-1
CC protein. The fusion proteins can be used to induce apoptosis in a tissue,
CC and to treat proliferative disorders, immune disorders, or virally-
CC induced disorders. The proliferative disorders include cancers, such as
CC breast, prostate, lung or colon cancer. The viral infections include
CC hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune
CC disorders may be autoimmune disorders or transplant rejection.
CC Cardiovascular diseases such as arteriosclerosis may also be treated. The
CC AGP-1 containing fusion proteins have increased biological activity
CC compared to the soluble AGP-1 proteins used in prior art therapies
XX
SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 3; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.6e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||| |:||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
```

RESULT 6
AAB80897
ID AAB80897 standard; protein; 232 AA.
XX
AC AAB80897;
XX
DT 31-MAY-2001 (first entry)
XX
DE Human IgGgamma1 hinge, CH2 and CH3 regions.
XX
KW Human; IgGgamma1; anticancer; Antimetastatic; Osteogenic;
KW lytic bone disease; multiple myeloma; immunoglobulin;
KW osteosclerotic bone metastasis; OPG; osteoprotegrin;
KW osteoclast formation inhibition; bone resorption inhibition.
XX
OS Homo sapiens.
XX
PN WO200117543-A2.
XX
PD 15-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-US022806.
XX
PR 03-SEP-1999; 99US-00389545.
XX
PA (AMGE-) AMGEN INC.
XX
PI Dunstan CR;
XX
DR WPI; 2001-265936/27.
XX
PT Preventing or treating lytic bone diseases, particularly associated with
PT cancer or metastasis, by administering an osteoprotegrin polypeptide.
XX
PS Disclosure; Fig 1; 87pp; English.
XX
CC The present invention relates to a method for the prevention or treatment
CC of lytic bone disease or multiple myeloma. Also the method can be used
CC for preventing metastasis of cancer to bone or osteosclerotic bone
CC metastasis. The method comprises administering an OPG (osteoprotegrin)
CC polypeptide or OPG fusion protein. The OPG proteins (see AAB80898-
CC AAB80905) can inhibit formation of osteoclasts (and thus bone resorption)
CC by blocking differentiation from monocytes/macrophage precursors. The
CC present sequence is the hinge, CH2 and CH3 regions of human IgGgamma1.
CC This sequence can be used to generate fusion proteins of OPG and
CC immunoglobulin, for use in the present invention. The generated fusion
CC proteins can exhibit increased circulating half-lives and slower
CC clearance times, thereby providing a more sustained activity
XX
SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 4; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.6e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||| |:||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
```

RESULT 7
AAY72915
ID AAY72915 standard; protein; 232 AA.
XX
AC AAY72915;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.
XX
KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
KW periodontal.
XX
OS Homo sapiens.
XX
PN WO200118203-A1.
XX
PD 15-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-US022797.
XX
PR 03-SEP-1999; 99US-00389782.
XX
PA (AMGE-) AMGEN INC.

Dunstan CR, Wooden SK, Mann MB;

WPI; 2001-244572/25.

Osteoprotegerin-Fc protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis.

Claim 3; Fig 1; 119pp; English.

The patent discloses fusion protein comprising human osteoprotegerin (OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively regulates formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion protein is administered for the treatment of bone loss resulting from osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia associated with surgery or steroid administration, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic loosening. The present sequence is partial human immunoglobulin G (Ig G) 1 protein comprising the hinge and heavy chain constant regions CH2 and CH3

Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 4; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.6e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||||:|:||||||||||||||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
```

RESULT 8
AAE15347
AAE15347 standard; protein; 232 AA.

AAE15347;

09-APR-2002 (first entry)

Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.

Human; erythropoietin; Epo; haematocrit; anaemia; kidney function; IgG; cancer; myelosuppressive therapy; anti-viral drug; immunoglobulin G.

Homo sapiens.

WO200181405-A2.

01-NOV-2001.

19-APR-2001; 2001WO-US012836.

21-APR-2000; 2000US-00559001.

(AMGE-) AMGEN INC.

Egrie JC, Elliott SG, Browne JK, Sitney KC;

WPI; 2002-034433/04.

Increasing and maintaining hematocrit in mammal suffering from anemia, comprising administering hyperglycosylated analog of erythropoietin less frequently and at lower molar amount of recombinant human erythropoietin.

PS Example 1; Fig 10; 95pp; English.

CC The invention relates to a method for increasing and maintaining haematocrit in a mammal. The method comprises administering a hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical composition, less frequently than an equivalent molar amount of and at a lower molar amount than recombinant human Epo (rHuEpo) to obtain a comparable target haematocrit. Epo is a glycoprotein hormone necessary for the maturation of erythroid progenitor cells into erythrocytes. Human Epo analogue is useful for raising and maintaining haematocrit to a comparable target haematocrit in a mammal suffering from anaemia associated with a decline or loss of kidney function, myelosuppressive therapy comprising chemotherapeutic or anti-viral drugs or associated with excessive blood loss during surgical procedures, and in cancer condition. The present sequence is human immunoglobulin G (IgG) gamma 1 constant heavy chain (CH2, CH3) hinge region used to construct Epo hyperglycosylated analogue fusion protein

SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.6e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||||:|:||||||||||||||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
```

RESULT 9
AAE26272
ID AAE26272 standard; protein; 232 AA.

AC AAE26272;

DT 14-NOV-2002 (first entry)

DE Human IgG1 heavy chain.

KW Human; amyloidogenic protein; Alzheimer's disease; Huntington's disease; spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis; Gerstmann-Straussler-Scheinker syndrome; spongiform encephalopathy; GSS; Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma; CJ.

OS Homo sapiens.

PN WO200242462-A2.

PD 30-MAY-2002.

PF 27-NOV-2001; 2001WO-US044581.

PR 27-NOV-2000; 2000US-0253302P.
PR 29-NOV-2000; 2000US-0250198P.

```
PR   20-DEC-2000; 2000US-0257186P.
XX
PA   (PRAE-) PRAECIS PHARM INC.
XX
PI   Gefter ML,  Israel DI,  Joyal JL,  Gosselin M;
XX
DR   WPI; 2002-636427/68.
XX
PT   Novel therapeutic agent useful for treating an amyloidogenic disorder,
PT   e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain
PT   constant region linked to a peptide capable of binding amyloidogenic
PT   protein.
XX
PS   Example 8; Page 76; 79pp; English.
XX
CC   The invention relates to a compound comprising an immunoglobulin (Ig)
CC   heavy chain constant region or its fragment that retains the ability to
CC   bind an Fc receptor linked by a linker group or a direct bond to a
CC   peptide capable of binding an amyloidogenic protein. The invention is
CC   useful for clearing an amyloidogenic protein such as beta-amyloid,
CC   transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide
CC   (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda light
CC   chain, amyloid A, procalcitonin, cystatin C, beta2-microglobulin, ApoA-I,
CC   gelsolin, calcitonin, fibrinogen, Huntington, alpha-synuclein and
CC   lysozyme from a subject and for treating an amyloidogenic disorder such
CC   as Alzheimer's disease and spongiform encephalopathy. Disorders treatable
CC   include those caused or characterised by deposits of TTR (eg. familial
CC   amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies, including
CC   scrapie in sheep, bovine spongiform encephalopathy in cows and
CC   Creutzfeldt-Jacob disease (CJ) and Gerstmann-Straussler-Scheinker
CC   syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes),
CC   ANF (eg. isolated atrial amyloid), kappa or lambda light chain (eg.
CC   idiopathic amyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I
CC   (eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg.
CC   familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal
CC   amyloidosis), Lysozyme (eg. hereditary systemic amyloidosis). Other
CC   examples of amyloidogenic disorders include Huntington's disease and
CC   inclusion body myocytis. The present sequence is human IgG1 heavy chain,
CC   used in the exemplification of the invention
XX
SQ   Sequence 232 AA;

  Query Match             97.2%;  Score 1225;  DB 5;  Length 232;
  Best Local Similarity   97.0%;  Pred. No. 1.6e-88;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||:|:||||||||||||||||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||| |:||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232


RESULT 10
ADJ65991
ID   ADJ65991 standard; protein; 232 AA.
XX
AC   ADJ65991;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Herpes virus entry mediator-related protein #2.
XX
KW   therapeutic agent; endotoxin induced disease; fusion protein;
KW   Herpes virus entry mediator; HVEM; immunoglobulin Fc domain;
KW   endotoxic shock; human.
XX
OS   Homo sapiens.
XX
PN   JP2003128576-A.
XX
PD   08-MAY-2003.
XX
PF   25-OCT-2001; 2001JP-00328430.
XX
PR   25-OCT-2001; 2001JP-00328430.
XX
PA   (TAIS ) TAISHO PHARM CO LTD.
PA   (GENE-) GENE TECHNO SCI KK.
XX
DR   WPI; 2003-817833/77.
DR   N-PSDB; ADJ65998.
XX
PT   New therapeutic agent, useful for treating endotoxin induced disease,
PT   comprises fusion protein of Herpes virus entry mediator protein and
PT   immunoglobulin.
XX
PS   Claim 5; SEQ ID NO 2; 11pp; Japanese.
XX
CC   The invention comprises a therapeutic agent for treating endotoxin
CC   induced disease, the therapeutic agent contains a fusion protein of the
CC   Herpes virus entry mediator (HVEM) protein and an immunoglobulin Fc
CC   domain. The therapeutic agent of the invention is useful for treating
CC   endotoxin induced disease, such as endotoxic shock. The present amino
CC   acid sequence represents a human protein which is claimed in the
CC   specification.
XX
SQ   Sequence 232 AA;

  Query Match             97.2%;  Score 1225;  DB 7;  Length 232;
  Best Local Similarity   97.0%;  Pred. No. 1.6e-88;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||:|:||||||||||||||||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||| |:||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232


RESULT 11
ADJ57512
ID   ADJ57512 standard; protein; 232 AA.
XX
AC   ADJ57512;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human IgG1 Fc domain fragment.
XX
KW   TF; tissue factor; FVIIa; factor VII; anticoagulant; thrombolytic;
KW   cerebroprotective; cytostatic; vasotropic; antirheumatic; antiarthritic;
KW   antiarteriosclerotic; antiinflammatory; antibacterial; immunosuppressive;
KW   hypertensive; cardiant; coagulation Factor VII; human; immunoglobulin G1;
KW   IgG1.
XX
```

Homo sapiens.

WO2004006962-A2.

22-JAN-2004.

09-JUL-2003; 2003WO-DK000481.

12-JUL-2002; 2002DK-00001099.

(NOVO) NOVO NORDISK AS.

Bjorn SE, Nicolaisen EM, Steenstrup TD;

WPI; 2004-180224/17.

New compound binding to tissue factor, useful for treating diseases such as angiogenesis, ischemia/reperfusion, and rheumatoid arthritis.

Claim 16; SEQ ID NO 7; 61pp; English.

The invention relates to a compound (I) binding to tissue factor (TF). The compound (I) has the formula A-(LM)-C, where A is a FVIIa polypeptide, LM is an optional linker group, C comprises an immunostimulatory effector domain, and (I) binds to TF. (I) inhibits TF-mediated activated factor VII (FVIIa) activity. (I) is useful as a medicament, and for the manufacture of a medicament for preventing or treating disease or disorder associated with pathophysiological TF activity. The disease or disorder associated with pathophysiological TF activity are deep venous thrombosis, arterial thrombosis, post surgical thrombosis, coronary artery bypass graft (CABG), percutaneous transdermal coronary angioplastry (PTCA), stroke, cancer, tumor metastasis, angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolysis, arteriosclerosis and restenosis following angioplastry, acute and chronic indications such as inflammation, septic shock, septicemia, hypotension, adult respiratory distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial infarction, or prophylactic treatment of mammals with atherosclerotic vessels at risk for thrombosis. The present sequence represents the Fc domain fragment of human immunoglobulin G1 (IgG1).

Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.6e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
y          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

y         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
            |||||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||
b         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

y        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
b        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

y        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
            ||||| |||||||||||||||||||||||||||||||| |:||||||||
b        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
```

ESULT 12
BB09463
D ABB09463 standard; protein; 233 AA.
X
C ABB09463;
X
T 01-JUL-2002 (first entry)
X
E Human IgG Fc fragment amino acid sequence.

XX
KW Protein A; immunoglobin G; IgG; antibody; human.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Misc-difference 168
FT /note= "encoded by GAC"
FT Misc-difference 169
FT /note= "encoded by ACC"
XX
PN WO200204602-A1.
XX
PD 17-JAN-2002.
XX
PF 04-JUL-2001; 2001WO-JP005788.
XX
PR 07-JUL-2000; 2000JP-00206689.
XX
PA (GENC-) GENCOM CORP.
XX
PI Tanaka A, Ueda M, Teranishi Y;
XX
DR WPI; 2002-148174/19.
DR N-PSDB; ABL52834.
XX
PT Transformant yeast for stable supply of highly active catalytic antibody,
PT comprises the capability of expressing and presenting protein A or its
PT fragment, particularly with the ZZ domain, on the cell surface.
XX
PS Example 3; Fig 4; 25pp; Japanese.
XX
CC The invention relates to a transformant yeast that can present protein A
CC or its fragment on its cell surface. The yeast can be used for detecting
CC or isolating the Fc part of immunoglobulin (Ig)G. The yeast is useful for
CC a stable supply of highly active catalytic antibody e.g. by screening
CC novel functional molecules and in isolating Fc-carrying secretory
CC proteins. The yeast of the invention is capable of adhering specifically
CC to a combinatorial antibody library with an Fc-carrying antibody
CC component. The current sequence represents the human IgG Fc fragment
CC amino acid sequence
XX
SQ Sequence 233 AA;

Query Match 97.2%; Score 1225; DB 5; Length 233;
Best Local Similarity 97.0%; Pred. No. 1.6e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy         1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 61

Qy        61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
            |||||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||
Db        62 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 121

Qy       121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       122 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 181

Qy       181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
            ||||| |||||||||||||||||||||||||||||||| |:||||||||
Db       182 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 233
```

RESULT 13
ABJ38647
ID ABJ38647 standard; protein; 235 AA.
XX
AC ABJ38647;
XX
DT 26-JUN-2003 (first entry)
XX

DE pCXFc protein SEQ ID No 6.
XX
KW Cytostatic; osteopathic; cerebroprotective; dermatological; enzyme;
KW antigen binding; receptor protein tyrosine kinase; skeletal dysplasia;
KW constitutive activation; craniosynostosis; cell proliferative disorder;
KW achondroplasia; thanatophoric dysplasia; acanthosis nigricans dysplasia;
KW hypochondroplasia; severe achondroplasia; transitional cell carcinoma;
KW Muenke coronal craniosynostosis; Crouzin syndrome; acanthosis nigricans;
KW tumour progression; osteosarcoma; chondrosarcoma; multiple myeloma;
KW mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein.
XX
OS Homo sapiens.
XX
PN WO2002102854-A2.
XX
PD 27-DEC-2002.
XX
PF 20-JUN-2002; 2002WO-IB003523.
XX
PR 20-JUN-2001; 2001US-0299187P.
XX
PA (MORP-) MORPHOSYS AG.
PA (PROC-) PROCHON BIOTECH LTD.
XX
PI Thomassen-Wolf E, Borges E, Yayon A, Rom E;
XX
DR WPI; 2003-167489/16.
DR N-PSDB; ABT40262.
XX
PT New molecules having the antigen-binding portion of antibodies that block
PT activation of receptor protein tyrosine kinase, useful for treating or
PT inhibiting skeletal dysplasias, craniosynostosis or cell proliferative
PT disorders.
XX
PS Example 2; Page 38; 103pp; English.
XX
CC The invention relates to a novel molecule comprising the antigen binding
CC portion of an isolated antibody, which has an increased affinity for a
CC receptor protein tyrosine kinase and which blocks constitutive activation
CC of the receptor protein tyrosine kinase. The methods and compositions of
CC the invention are useful for treating or inhibiting a skeletal dysplasia,
CC craniosynostosis or a cell proliferative disorder. The skeletal dysplasia
CC is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe
CC achondroplasia with developmental delay or acanthosis nigricans
CC dysplasia. The craniosynostosis disorder is Muenke coronal
CC craniosynostosis or Crouzin syndrome with acanthosis nigricans. The cell
CC proliferative disorder is tumour progression that is progression of
CC transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple
CC myeloma or mammary carcinoma. This sequence represents a protein derived
CC from a pCXFc plasmid DNA vector relating to the protein tyrosine kinase
CC inhibitor of the invention
XX
SQ Sequence 235 AA;

Query Match 97.2%; Score 1225; DB 6; Length 235;
Best Local Similarity 97.0%; Pred. No. 1.6e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 63

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||:|:|||||||||||||||||||||
Db         64 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 123

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 183

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        184 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 235
```

RESULT 14
ADA89055
ID ADA89055 standard; protein; 235 AA.
XX
AC ADA89055;
XX
DT 20-NOV-2003 (first entry)
XX
DE Plasmid pCXFc amino acid sequence SEQ ID NO:6.
XX
KW antigen binding; antibody; specific binding affinity;
KW receptor protein tyrosine kinase; RPTK;
KW receptor protein tyrosine kinase inhibitor;
KW fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;
KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;
KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;
KW hypochondroplasia; craniosynostosis disorder;
KW malignant cell proliferative disease; cancer; tumour; vision disorder;
KW non-neoplastic angiogenic pathologic condition.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2002102973-A2.
XX
PD 27-DEC-2002.
XX
PF 20-JUN-2002; 2002WO-IL000495.
XX
PR 20-JUN-2001; 2001US-0299187P.
XX
PA (PROC-) PROCHON BIOTECH LTD.
XX
PI Yayon A, Rom E;
XX
DR WPI; 2003-175236/17.
DR N-PSDB; ADA89054.
XX
PT New antibodies which have specific binding affinity for a receptor
PT protein tyrosine kinase (RPTK) and block constitutive activation of RPTK,
PT useful for treating bone and cartilage disorders, or malignant cell
PT proliferative diseases.
XX
PS Example 2; Page 43; 122pp; English.
XX
CC The present invention describes a molecule (I) comprising the antigen
CC binding portion of an isolated antibody which has specific binding
CC affinity for a receptor protein tyrosine kinase (RPTK), particularly for
CC a fibroblast growth factor receptor (FGFR), and which blocks constitutive
CC activation of an RPTK. Also described: (1) pharmaceutical compositions
CC comprising (I) as an active ingredient and a pharmaceutical carrier,
CC excipient, or auxiliary agent; (2) a kit comprising (I), at least one
CC reagent for detecting the presence of (I) when bound to the RPTK, and
CC instructions for use; (3) a method for treatment of bone and cartilage
CC related disorders by administering a composition of (1) to the subject;
CC (4) a method for treating or inhibiting a cell proliferative disease or
CC disorder by administering the composition of (1); (5) a method for
CC screening a molecule comprising the antigen-binding portion of an
CC antibody which blocks ligand-dependent activation of RPTK; (6) an
CC isolated nucleic acid molecule encoding a VL-CDR3 DNA region and a VH-
CC CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VL region
CC and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or
CC (7); and (9) host cells transformed with the vector. (I) have
CC osteopathic, cytostatic and ophthalmological activities, and can be used
CC as a RPTK inhibitor. Compositions comprising (I) are useful for treating
CC bone and cartilage disorders, including skeletal disorders such as
CC skeletal dysplasia (achondroplasia, thanatophoric dysplasia,
CC hypochondroplasia, severe achondroplasia with developmental delay and
CC acanthosis nigricans dysplasia) or a craniosynostosis disorder (e.g.
CC Muenke coronal craniosynostosis or Crouzon syndrome with acanthosis
CC nigricans). The composition may also be used for treating or inhibiting

malignant cell proliferative disease or disorder associated with abnormal RPTK activity, including a haematopoietic malignancy (e.g. multiple myeloma), solid tumours (e.g. mammary, colon, cervical, bladder, colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary tumours, tumour progression (particularly progression of transitional cell carcinoma or mammary carcinoma), or tumour metastasis, where the cell proliferative disorder may be associated with the action of a constitutively activated RPTK, or with ligand-dependent activation of RPTK. The compositions may further be used for treating hyperproliferative diseases and disorders associated with ligand-dependent FGFR signaling, such as vision disorders (e.g. neovascular glaucoma, macular degeneration and proliferative retinopathy including diabetic retinopathy), and non-neoplastic angiogenic pathologic conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present sequence is given in the exemplification of the present invention.

Sequence 235 AA;

Query Match 97.2%; Score 1225; DB 6; Length 235;
Best Local Similarity 97.0%; Pred. No. 1.6e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 63

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||
Db         64 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 123

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 183

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| ||||||||||||||||||||||||||||||||||| :||||||||
Db        184 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 235
```

RESULT 15
ADD25647
ID ADD25647 standard; protein; 235 AA.
XX
AC ADD25647;
XX
DT 15-JAN-2004 (first entry)
XX
DE Binding domain-immunoglobulin fusion protein-associated protein #101.
XX
KW Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS Unidentified.
XX
PN US2003118592-A1.
XX
PD 26-JUN-2003.
XX
PF 25-JUL-2002; 2002US-00207655.
XX
PR 17-JAN-2001; 2001US-0367358P.
PR 17-JAN-2002; 2002US-00053530.
PR 03-JUN-2002; 2002US-0385691P.
XX
PA (GENE-) GENECRAFT INC.
XX
IN Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
DR WPI; 2003-801317/75.
XX
PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 208; 157pp; English.
XX
CC The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide, derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX
SQ Sequence 235 AA;

Query Match 97.2%; Score 1225; DB 7; Length 235;
Best Local Similarity 97.0%; Pred. No. 1.6e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 63

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||||:|:||||||||||||||||||||
Db         64 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 123

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 183

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| ||||||||||||||||||||||||||||||||||| :||||||||
Db        184 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 235
```

Search completed: October 27, 2004, 16:59:37
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protein - protein search, using sw model

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Maximum Match 100%
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	% Query Match	Length	DB	ID	Description
1	1260	100.0	232	10	US-09-847-208-3	Sequence 3, Appli
2	1260	100.0	232	14	US-10-000-439-3	Sequence 3, Appli
3	1260	100.0	330	10	US-09-847-208-2	Sequence 2, Appli
4	1260	100.0	330	14	US-10-000-439-2	Sequence 2, Appli
5	1260	100.0	569	10	US-09-847-208-7	Sequence 7, Appli
6	1260	100.0	569	14	US-10-000-439-7	Sequence 7, Appli
7	1225	97.2	232	9	US-09-996-357-10	Sequence 10, Appl
8	1225	97.2	232	10	US-09-389-782-1	Sequence 1, Appli
9	1225	97.2	232	16	US-10-617-619-7	Sequence 7, Appli
10	1225	97.2	232	16	US-10-761-593A-26	Sequence 26, Appl
11	1225	97.2	235	14	US-10-207-655-208	Sequence 208, App
12	1225	97.2	247	9	US-09-996-357-13	Sequence 13, Appl
13	1225	97.2	251	14	US-10-008-063-18	Sequence 18, Appl
14	1225	97.2	251	14	US-10-152-363A-6	Sequence 6, Appli
15	1225	97.2	267	9	US-09-996-357-12	Sequence 12, Appl
16	1225	97.2	288	10	US-09-822-851B-14	Sequence 14, Appl
17	1225	97.2	288	14	US-10-119-637A-14	Sequence 14, Appl
18	1225	97.2	329	15	US-10-370-749-48	Sequence 48, Appl
19	1225	97.2	330	10	US-09-995-898A-15	Sequence 15, Appl
20	1225	97.2	330	10	US-09-892-949-38	Sequence 38, Appl
21	1225	97.2	330	13	US-10-047-542-20	Sequence 20, Appl
22	1225	97.2	330	14	US-10-269-805-68	Sequence 68, Appl
23	1225	97.2	330	14	US-10-310-719-8	Sequence 8, Appli
24	1225	97.2	330	14	US-10-112-582-1	Sequence 1, Appli
25	1225	97.2	330	14	US-10-320-231A-81	Sequence 81, Appl
26	1225	97.2	330	14	US-10-383-902A-6	Sequence 6, Appli
27	1225	97.2	330	15	US-10-408-901-2	Sequence 2, Appli
28	1225	97.2	330	15	US-10-420-034A-15	Sequence 15, Appl
29	1225	97.2	330	15	US-10-257-907-5	Sequence 5, Appli
30	1225	97.2	330	15	US-10-656-769-2	Sequence 2, Appli
31	1225	97.2	330	16	US-10-679-620-58	Sequence 58, Appl
32	1225	97.2	330	16	US-10-772-531-38	Sequence 38, Appl
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34	1225	97.2	331	9	US-09-761-413-2	Sequence 2, Appli
35	1225	97.2	331	14	US-10-341-836-2	Sequence 2, Appli
36	1225	97.2	332	10	US-09-990-586-98	Sequence 98, Appl
37	1225	97.2	332	14	US-10-310-113-167	Sequence 167, App
38	1225	97.2	332	14	US-10-230-880-98	Sequence 98, Appl
39	1225	97.2	333	15	US-10-272-899A-8	Sequence 8, Appli
40	1225	97.2	356	15	US-10-272-899A-72	Sequence 72, Appl
41	1225	97.2	358	14	US-10-233-150-5	Sequence 5, Appli
42	1225	97.2	360	9	US-09-949-713-11	Sequence 11, Appl
43	1225	97.2	367	15	US-10-452-646-9	Sequence 9, Appli
44	1225	97.2	371	14	US-10-157-408-7	Sequence 7, Appli
45	1225	97.2	371	14	US-10-097-044A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-847-208-3
; Sequence 3, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IgE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-3

Query Match 100.0%; Score 1260; DB 10; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.8e-93;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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Db         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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Db        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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RESULT 2
US-10-000-439-3
; Sequence 3, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-3

Query Match 100.0%; Score 1260; DB 14; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.8e-93;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-847-208-2
; Sequence 2, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IgE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-2

Query Match 100.0%; Score 1260; DB 10; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.5e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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Db        219 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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RESULT 4
US-10-000-439-2
; Sequence 2, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-2

Query Match 100.0%; Score 1260; DB 14; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.5e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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RESULT 5
US-09-847-208-7
; Sequence 7, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IgE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177

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 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
  LENGTH: 569
  TYPE: PRT
  ORGANISM: Unknown
  FEATURE:
  OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4
  OTHER INFORMATION: (IgE)
-09-847-208-7

Query Match            100.0%;  Score 1260;  DB 10;  Length 569;
Best Local Similarity   100.0%;  Pred. No. 2.8e-92;
Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120

        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
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SULT 6
-10-000-439-7
 Sequence 7, Application US/10000439
 Publication No. US20030064063A1
 GENERAL INFORMATION:
  APPLICANT: Saxon, Andrew
  TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
  TITLE OF INVENTION:  TREATMENT OF IMMUNE DISEASES
  FILE REFERENCE: UC067.004A
  CURRENT APPLICATION NUMBER: US/10/000,439
  CURRENT FILING DATE:  2001-10-24
  PRIOR APPLICATION NUMBER: US 09/847,208
  PRIOR FILING DATE: 2001-05-01
  NUMBER OF SEQ ID NOS: 13
  SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 7
   LENGTH: 569
   TYPE: PRT
   ORGANISM: Unknown
   FEATURE:
   OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3
   OTHER INFORMATION: (IgG1) sequence and a CH2-CH3-CH4 (IgE) sequence
-10-000-439-7

 Query Match            100.0%;  Score 1260;  DB 14;  Length 569;
 Best Local Similarity   100.0%;  Pred. No. 2.8e-92;
 Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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           1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

          61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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         121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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Db         181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232


RESULT 7
US-09-996-357-10
; Sequence 10, Application US/09996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
;  APPLICANT: Gefter, Malcolm L
;  APPLICANT:  Isreal, David I
;  APPLICANT:  Joyal, John L
;  APPLICANT:  Gosselin, Michael
;  TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
;  TITLE OF INVENTION:  TREATING AN AMYLOIDOGENIC DISEASE
;  FILE REFERENCE: PPI-105
;  CURRENT APPLICATION NUMBER: US/09/996,357
;  CURRENT FILING DATE:  2001-11-27
;  PRIOR APPLICATION NUMBER: 60/253,302
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/250,198
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: 60/257,186
;  PRIOR FILING DATE: 2000-12-20
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 232
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-996-357-10

  Query Match            97.2%;  Score 1225;  DB 9;  Length 232;
  Best Local Similarity   97.0%;  Pred. No. 6.1e-90;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
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Db           1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy          61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
               |||||||||||| |||||||||||||||||||:|:||||||||||||||||||||||||
Db          61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy         121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy         181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
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Db         181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232


RESULT 8
US-09-389-782-1
; Sequence 1, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
;  APPLICANT: Wooden, Scott K.
;  APPLICANT: Mann, Michael B.
;  APPLICANT: Dunstan, Colin R.
;  TITLE OF INVENTION: CPG Fusion Protein Compositions and Methods
;  FILE REFERENCE: A-604
;  CURRENT APPLICATION NUMBER: US/09/389,782
;  CURRENT FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 232
;   TYPE: PRT
;   ORGANISM: Human
US-09-389-782-1

  Query Match            97.2%;  Score 1225;  DB 10;  Length 232;
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Best Local Similarity 97.0%; Pred. No. 6.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
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Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
```

RESULT 9
US-10-617-619-7
; Sequence 7, Application US/10617619
; Publication No. US20040110929A1
; GENERAL INFORMATION:
; APPLICANT: Bjorn, Soren E
; APPLICANT: Nicolaisen, Else M
; APPLICANT: Jorgensen, Anker S
; TITLE OF INVENTION: TF Binding Compound
; FILE REFERENCE: 6455.200-US
; CURRENT APPLICATION NUMBER: US/10/617,619
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/404,568
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human
US-10-617-619-7

Query Match 97.2%; Score 1225; DB 16; Length 232;
Best Local Similarity 97.0%; Pred. No. 6.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||||:|:||||||||||||||||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
```

RESULT 10
US-10-761-593A-26
; Sequence 26, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-761-593A-26

Query Match 97.2%; Score 1225; DB 16; Length 232;
Best Local Similarity 97.0%; Pred. No. 6.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||||:|:||||||||||||||||||||||||
Db         61 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        181 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
```

RESULT 11
US-10-207-655-208
; Sequence 208, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 208
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide
US-10-207-655-208

Query Match 97.2%; Score 1225; DB 14; Length 235;
Best Local Similarity 97.0%; Pred. No. 6.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 63

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||||:|:||||||||||||||||||||||||
Db         64 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 123

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 183
```

```
Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||||||| |:||||||||
Db        184 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 235
```

RESULT 12
US-09-996-357-13
Sequence 13, Application US/09996357
Patent No. US20020133001A1
GENERAL INFORMATION:
APPLICANT: Gefter, Malcolm L
APPLICANT: Isreal, David I
APPLICANT: Joyal, John L
APPLICANT: Gosselin, Michael
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
FILE REFERENCE: PPI-105
CURRENT APPLICATION NUMBER: US/09/996,357
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,302
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/250,198
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/257,186
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-357-13

Query Match 97.2%; Score 1225; DB 9; Length 247;
Best Local Similarity 97.0%; Pred. No. 6.6e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 75

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||
Db         76 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 135

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 195

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| ||||||||||||||||||||||||||||||||| |:||||||||
Db        196 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 247
```

RESULT 13
US-10-008-063-18
Sequence 18, Application US/10008063
Publication No. US20030092164A1
GENERAL INFORMATION:
APPLICANT: Gross, Jane A.
APPLICANT: Xu, Wenfeng
APPLICANT: Henne, Randal M.
APPLICANT: Grant, Francis, J.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REFERENCE: 00-103
CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-10-008-063-18

Query Match 97.2%; Score 1225; DB 14; Length 251;
Best Local Similarity 97.0%; Pred. No. 6.7e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 79

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||
Db         80 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 139

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 199

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| ||||||||||||||||||||||||||||||||| |:||||||||
Db        200 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 251
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RESULT 14
US-10-152-363A-6
; Sequence 6, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-152-363A-6

Query Match 97.2%; Score 1225; DB 14; Length 251;
Best Local Similarity 97.0%; Pred. No. 6.7e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 79

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||||| ||||||||||||||||||||||:|:||||||||||||||||||||||
Db         80 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 139

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 199

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| ||||||||||||||||||||||||||||||||| |:||||||||
Db        200 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 251
```

RESULT 15
US-09-996-357-12
; Sequence 12, Application US/09996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
; APPLICANT: Gefter, Malcolm L
; APPLICANT: Isreal, David I
; APPLICANT: Joyal, John L

```
;  APPLICANT:  Gosselin, Michael
;  TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
;  TITLE OF INVENTION:  TREATING AN AMYLOIDOGENIC DISEASE
;  FILE REFERENCE: PPI-105
;  CURRENT APPLICATION NUMBER: US/09/996,357
;  CURRENT FILING DATE:  2001-11-27
;  PRIOR APPLICATION NUMBER: 60/253,302
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/250,198
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: 60/257,186
;  PRIOR FILING DATE: 2000-12-20
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:alpha-beta(16-30)Fc
US-09-996-357-12

  Query Match           97.2%;  Score 1225;  DB 9;  Length 267;
  Best Local Similarity   97.0%;  Pred. No. 7.2e-90;
  Matches  225;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 95

Qy         61 NWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKT 120
              |||||||||| |||||||||||||||||||||:|:||||||||||||||||||||||||
Db         96 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 155

Qy        121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 215

Qy        181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSLSPGK 232
              ||||| |||||||||||||||||||||||||||||| |:||||||||
Db        216 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 267


Search completed: October 27, 2004, 17:20:19
Job time : 72.0036 secs
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